```
ile 155:MEDLINE(R)  1966-2003/Nov W2
       (c) format only 2003 The Dialog Corp.
*File 155: On 13 November, Medline will temporarily stop updating with
Completed records. Please see HELP NEWS 154 for details.

      Set  Items  Description
      ---  -----  -----------
Cost is in DialUnits
?ds

Set      Items   Description
S1       10402   'SERINE PROTEASES' OR 'SERINE ENDOPEPTIDASES'
S2       37019   R1-R5
S3         332   'ENTEROPEPTIDASE'
S4       14699   E3-E12
S5       11239   E13-E50
S6        2796   E1-E50
S7          76   (S1 OR S2 OR S3) AND (S4 OR S5 OR S6)
S8          43   S7/1997:2003
S9          33   S7 NOT S8
S10         23   S9 AND SERINE?
?e ausp

Ref   Items  Index-term
E1        2  AUSONIA
E2        6  AUSONICS
E3        5 *AUSP
E4        1  AUSPAP
E5        1  AUSPERATE
E6        3  AUSPHARM
E7        1  AUSPICA
E8        1  AUSPICABILE
E9        1  AUSPICABILI
E10       2  AUSPICABLE
E11       1  AUSPICARE
E12       4  AUSPICATE

          Enter P or PAGE for more
?s e3
```

```
## Status: Break Sent.

?e serine protease

Ref    Items    RT  Index-term
E1         0     1  SERINE PHOSPHATE
E2         0     1  SERINE PHOSPHOGLYCERIDES
E3         0       *SERINE PROTEASE
E4         1       SERINE PROTEASE APRM
E5        22       SERINE PROTEASE INHIBITOR 2.1
E6         5       SERINE PROTEASE INHIBITOR 2.3
E7         5       SERINE PROTEASE INHIBITOR 3
E8         0     1  SERINE PROTEASE INHIBITORS
E9         6       SERINE PROTEASE PB92
E10        1       SERINE PROTEASE TESP5, MOUSE
E11        0     1  SERINE PROTEASES
E12        0     1  SERINE PROTEINASE ANTAGONISTS

          Enter P or PAGE for more
?p

Ref    Items    RT  Index-term
E13        1       SERINE PROTEINASE INHIBITOR IA-1
E14        1       SERINE PROTEINASE INHIBITOR IA-2
E15     3755    28  SERINE PROTEINASE INHIBITORS
E16      151       SERINE PROTEINASE INHIBITORS --ADMINISTRATION
E17       31       SERINE PROTEINASE INHIBITORS --ADVERSE EFFECTS
E18      127       SERINE PROTEINASE INHIBITORS --ANALYSIS --AN
E19       90       SERINE PROTEINASE INHIBITORS --BIOSYNTHESIS --
E20      155       SERINE PROTEINASE INHIBITORS --BLOOD --BL
E21      243       SERINE PROTEINASE INHIBITORS --CHEMICAL SYNTHE
E22      733       SERINE PROTEINASE INHIBITORS --CHEMISTRY --CH
E23       11       SERINE PROTEINASE INHIBITORS --CLASSIFICATION
E24       19       SERINE PROTEINASE INHIBITORS --DEFICIENCY --DF

          Enter P or PAGE for more
?e e11

Ref    Items Type  RT  Index-term
R1         0        1 *SERINE PROTEASES
R2     10402   X   37  SERINE ENDOPEPTIDASES
?s r1 or r2
               0  SERINE PROTEASES
           10402  SERINE ENDOPEPTIDASES
      S1   10402  'SERINE PROTEASES' OR 'SERINE ENDOPEPTIDASES'
?e r2

Ref    Items Type  RT  Index-term
R1     10402       37 *SERINE ENDOPEPTIDASES
R2     10402   X      DC=D8.586.277.656.300.760. (SERINE ENDOPEPTIDASES)
R3         0   X    1  SERINE PROTEASES
R4         0   X    1  SERINE PROTEINASES
R5     37019   B   75  ENDOPEPTIDASES
R6       776   N    3  ACROSIN
R7       432   N    8  ANCROD
R8       468   N   10  ANISTREPLASE
R9       383   N    9  BATROXOBIN
R10    16037   N    3  CHYMOTRYPSIN
R11     1127   N   12  COMPLEMENT FACTOR B
R12      199   N   12  COMPLEMENT FACTOR D

          Enter P or PAGE for more
?s r1-r5
           10402  SERINE ENDOPEPTIDASES
           10402  DC=D8.586.277.656.300.760.  (SERINE ENDOPEPTIDASES)
               0  SERINE PROTEASES
               0  SERINE PROTEINASES
           37019  ENDOPEPTIDASES
      S2   37019  R1-R5
```

```
?p

Ref    Items Type  RT  Index-term
R13      124   N    5  COMPLEMENT FACTOR I
R14     1202   N    3  ENDOPEPTIDASE K
R15      332   N    2  ENTEROPEPTIDASE
R16      371   N    8  FACTOR IXA
R17     1006   N    8  FACTOR VIIA
R18     2328   N   10  FACTOR XA
R19      159   N    8  FACTOR XIA
R20      288   N    8  FACTOR XIIA
R21     6121   N   14  KALLIKREINS
R22     1920   N    6  LEUKOCYTE ELASTASE
R23     6408   N    5  PANCREATIC ELASTASE
R24       23   N    3  PLASMA KALLIKREIN

          Enter P or PAGE for more
?s r15
      S3     332  'ENTEROPEPTIDASE'
?p

Ref    Items Type  RT  Index-term
R25     9683   N    4  PLASMIN
R26     5985   N    9  PLASMINOGEN ACTIVATORS
R27     1562   N    7  PREKALLIKREIN
R28     5769   N    4  PRONASE
R29     7745   N   12  PROSTATE-SPECIFIC ANTIGEN
R30     8814   N    8  STREPTOKINASE
R31     2518   N    2  SUBTILISIN
R32     2701   N    3  SUBTILISINS
R33    28692   N    8  THROMBIN
R34      319   N   11  TISSUE KALLIKREINS
R35     9208   N   13  TISSUE PLASMINOGEN ACTIVATOR
R36    54543   N    3  TRYPSIN

          Enter P or PAGE for more
?p

Ref    Items Type  RT  Index-term
R37     7873   N   10  URINARY PLASMINOGEN ACTIVATOR
R38        0   N    4  VENOMBIN A
?p
>>>Related terms display completed...
?ds

Set     Items   Description
S1      10402   'SERINE PROTEASES' OR 'SERINE ENDOPEPTIDASES'
S2      37019   R1-R5
S3        332   'ENTEROPEPTIDASE'
?e neisseria

Ref    Items   RT  Index-term
E1         1       NEISSEREAL
E2         1       NEISSERI
E3     14699   10 *NEISSERIA
E4        44       NEISSERIA --ANALYSIS --AN
E5         1       NEISSERIA --BLOOD --BL
E6         1       NEISSERIA --CEREBROSPINAL FLUID --CF
E7        15       NEISSERIA --CHEMISTRY --CH
E8       179       NEISSERIA --CLASSIFICATION --CL
E9        27       NEISSERIA --CYTOLOGY --CY
E10      207       NEISSERIA --DRUG EFFECTS --DE
E11      139       NEISSERIA --ENZYMOLOGY --EN
E12      155       NEISSERIA --GENETICS --GE

          Enter P or PAGE for more
?s e3-e12
          14699  NEISSERIA
             44  NEISSERIA --ANALYSIS --AN
```

```
              1  NEISSERIA --BLOOD --BL
              1  NEISSERIA --CEREBROSPINAL FLUID --CF
             15  NEISSERIA --CHEMISTRY --CH
            179  NEISSERIA --CLASSIFICATION --CL
             27  NEISSERIA --CYTOLOGY --CY
            207  NEISSERIA --DRUG EFFECTS --DE
            139  NEISSERIA --ENZYMOLOGY --EN
            155  NEISSERIA --GENETICS --GE
      S4  14699  E3-E12
?p

Ref    Items   RT  Index-term
E13       84       NEISSERIA --GROWTH AND DEVELOPMENT --GD
E14      155       NEISSERIA --IMMUNOLOGY --IM
E15      509       NEISSERIA --ISOLATION AND PURIFICATION --IP
E16      148       NEISSERIA --METABOLISM --ME
E17      125       NEISSERIA --PATHOGENICITY --PY
E18       24       NEISSERIA --PHYSIOLOGY --PH
E19        4       NEISSERIA --RADIATION EFFECTS --RE
E20       11       NEISSERIA --ULTRASTRUCTURE --UL
E21        1       NEISSERIA ADHERENCE-ASSOCIATED PROTEIN, HUMAN
E22     6150    4  NEISSERIA GONORRHOEAE
E23      149       NEISSERIA GONORRHOEAE --ANALYSIS --AN
E24       56       NEISSERIA GONORRHOEAE --CHEMISTRY --CH

         Enter P or PAGE for more
?p

Ref    Items   Index-term
E25      421   NEISSERIA GONORRHOEAE --CLASSIFICATION --CL
E26       71   NEISSERIA GONORRHOEAE --CYTOLOGY --CY
E27     1796   NEISSERIA GONORRHOEAE --DRUG EFFECTS --DE
E28      793   NEISSERIA GONORRHOEAE --ENZYMOLOGY --EN
E29     1056   NEISSERIA GONORRHOEAE --GENETICS --GE
E30      480   NEISSERIA GONORRHOEAE --GROWTH AND DEVELOPMENT
E31      836   NEISSERIA GONORRHOEAE --IMMUNOLOGY --IM
E32        1   NEISSERIA GONORRHOEAE --INSTRUMENTATION --IS
E33     2007   NEISSERIA GONORRHOEAE --ISOLATION AND PURIFICA
E34      491   NEISSERIA GONORRHOEAE --METABOLISM --ME
E35      312   NEISSERIA GONORRHOEAE --PATHOGENICITY --PY
E36      197   NEISSERIA GONORRHOEAE --PHYSIOLOGY --PH

         Enter P or PAGE for more
?p

Ref    Items   RT  Index-term
E37       13       NEISSERIA GONORRHOEAE --RADIATION EFFECTS --RE
E38      209       NEISSERIA GONORRHOEAE --ULTRASTRUCTURE --UL
E39     4777    9  NEISSERIA MENINGITIDIS
E40      112       NEISSERIA MENINGITIDIS --ANALYSIS --AN
E41        1       NEISSERIA MENINGITIDIS --CEREBROSPINAL FLUID -
E42      110       NEISSERIA MENINGITIDIS --CHEMISTRY --CH
E43      876       NEISSERIA MENINGITIDIS --CLASSIFICATION --CL
E44       27       NEISSERIA MENINGITIDIS --CYTOLOGY --CY
E45      604       NEISSERIA MENINGITIDIS --DRUG EFFECTS --DE
E46      180       NEISSERIA MENINGITIDIS --ENZYMOLOGY --EN
E47      709       NEISSERIA MENINGITIDIS --GENETICS --GE
E48      208       NEISSERIA MENINGITIDIS --GROWTH AND DEVELOPMEN

         Enter P or PAGE for more
?s e13-e50
             84  NEISSERIA --GROWTH AND DEVELOPMENT --GD
            155  NEISSERIA --IMMUNOLOGY --IM
            509  NEISSERIA --ISOLATION AND PURIFICATION --IP
            148  NEISSERIA --METABOLISM --ME
            125  NEISSERIA --PATHOGENICITY --PY
             24  NEISSERIA --PHYSIOLOGY --PH
              4  NEISSERIA --RADIATION EFFECTS --RE
             11  NEISSERIA --ULTRASTRUCTURE --UL
```

```
             1  NEISSERIA ADHERENCE-ASSOCIATED PROTEIN, HUMAN
          6150  NEISSERIA GONORRHOEAE
           149  NEISSERIA GONORRHOEAE --ANALYSIS --AN
            56  NEISSERIA GONORRHOEAE --CHEMISTRY --CH
           421  NEISSERIA GONORRHOEAE --CLASSIFICATION --CL
            71  NEISSERIA GONORRHOEAE --CYTOLOGY --CY
          1796  NEISSERIA GONORRHOEAE --DRUG EFFECTS --DE
           793  NEISSERIA GONORRHOEAE --ENZYMOLOGY --EN
          1056  NEISSERIA GONORRHOEAE --GENETICS --GE
           480  NEISSERIA GONORRHOEAE --GROWTH AND DEVELOPMENT
           836  NEISSERIA GONORRHOEAE --IMMUNOLOGY --IM
             1  NEISSERIA GONORRHOEAE --INSTRUMENTATION --IS
          2007  NEISSERIA GONORRHOEAE --ISOLATION AND PURIFICA
           491  NEISSERIA GONORRHOEAE --METABOLISM --ME
           312  NEISSERIA GONORRHOEAE --PATHOGENICITY --PY
           197  NEISSERIA GONORRHOEAE --PHYSIOLOGY --PH
            13  NEISSERIA GONORRHOEAE --RADIATION EFFECTS --RE
           209  NEISSERIA GONORRHOEAE --ULTRASTRUCTURE --UL
          4777  NEISSERIA MENINGITIDIS
           112  NEISSERIA MENINGITIDIS --ANALYSIS --AN
             1  NEISSERIA MENINGITIDIS --CEREBROSPINAL FLUID -
           110  NEISSERIA MENINGITIDIS --CHEMISTRY --CH
           876  NEISSERIA MENINGITIDIS --CLASSIFICATION --CL
            27  NEISSERIA MENINGITIDIS --CYTOLOGY --CY
           604  NEISSERIA MENINGITIDIS --DRUG EFFECTS --DE
           180  NEISSERIA MENINGITIDIS --ENZYMOLOGY --EN
           709  NEISSERIA MENINGITIDIS --GENETICS --GE
           208  NEISSERIA MENINGITIDIS --GROWTH AND DEVELOPMEN
          1658  NEISSERIA MENINGITIDIS --IMMUNOLOGY --IM
          1307  NEISSERIA MENINGITIDIS --ISOLATION AND PURIFIC
S5       11239  E13-E50
?p

Ref    Items  Index-term
E49     1658  NEISSERIA MENINGITIDIS --IMMUNOLOGY --IM
E50     1307  NEISSERIA MENINGITIDIS --ISOLATION AND PURIFIC
?p

Ref    Items   RT  Index-term
E1      1307       NEISSERIA MENINGITIDIS --ISOLATION AND PURIFIC
E2       310       NEISSERIA MENINGITIDIS --METABOLISM --ME
E3       348       NEISSERIA MENINGITIDIS --PATHOGENICITY --PY
E4       109       NEISSERIA MENINGITIDIS --PHYSIOLOGY --PH
E5         3       NEISSERIA MENINGITIDIS --RADIATION EFFECTS --R
E6        90       NEISSERIA MENINGITIDIS --ULTRASTRUCTURE --UL
E7         4       NEISSERIA MENINGITIDIS --VIROLOGY --VI
E8         9    4  NEISSERIA MENINGITIDIS, SEROGROUP A
E9         1       NEISSERIA MENINGITIDIS, SEROGROUP A --CLASSIFI
E10        2       NEISSERIA MENINGITIDIS, SEROGROUP A --GENETICS
E11        7       NEISSERIA MENINGITIDIS, SEROGROUP A --IMMUNOLO
E12        2       NEISSERIA MENINGITIDIS, SEROGROUP A --ISOLATIO

         Enter P or PAGE for more
?p

Ref    Items   RT  Index-term
E13        1       NEISSERIA MENINGITIDIS, SEROGROUP A --PATHOGEN
E14       21    4  NEISSERIA MENINGITIDIS, SEROGROUP B
E15        1       NEISSERIA MENINGITIDIS, SEROGROUP B --ENZYMOLO
E16        7       NEISSERIA MENINGITIDIS, SEROGROUP B --GENETICS
E17        1       NEISSERIA MENINGITIDIS, SEROGROUP B --GROWTH A
E18       14       NEISSERIA MENINGITIDIS, SEROGROUP B --IMMUNOLO
E19        4       NEISSERIA MENINGITIDIS, SEROGROUP B --ISOLATIO
E20        2       NEISSERIA MENINGITIDIS, SEROGROUP B --METABOLI
E21        6       NEISSERIA MENINGITIDIS, SEROGROUP B --PATHOGEN
E22       34    4  NEISSERIA MENINGITIDIS, SEROGROUP C
E23        1       NEISSERIA MENINGITIDIS, SEROGROUP C --CLASSIFI
E24        1       NEISSERIA MENINGITIDIS, SEROGROUP C --ENZYMOLO
```

```
          Enter P or PAGE for more
?p

Ref    Items   RT  Index-term
E25        4       NEISSERIA MENINGITIDIS, SEROGROUP C --GENETICS
E26        1       NEISSERIA MENINGITIDIS, SEROGROUP C --GROWTH A
E27       15       NEISSERIA MENINGITIDIS, SEROGROUP C --IMMUNOLO
E28       11       NEISSERIA MENINGITIDIS, SEROGROUP C --ISOLATIO
E29        2       NEISSERIA MENINGITIDIS, SEROGROUP C --METABOLI
E30        4       NEISSERIA MENINGITIDIS, SEROGROUP C --PATHOGEN
E31        9    3  NEISSERIA MENINGITIDIS, SEROGROUP W-135
E32        3       NEISSERIA MENINGITIDIS, SEROGROUP W-135 --CLAS
E33        2       NEISSERIA MENINGITIDIS, SEROGROUP W-135 --GENE
E34        2       NEISSERIA MENINGITIDIS, SEROGROUP W-135 --IMMU
E35        6       NEISSERIA MENINGITIDIS, SEROGROUP W-135 --ISOL
E36        4    4  NEISSERIA MENINGITIDIS, SEROGROUP Y

          Enter P or PAGE for more
?p

Ref    Items   RT  Index-term
E37        2       NEISSERIA MENINGITIDIS, SEROGROUP Y --CLASSIFI
E38        1       NEISSERIA MENINGITIDIS, SEROGROUP Y --DRUG EFF
E39        1       NEISSERIA MENINGITIDIS, SEROGROUP Y --ENZYMOLO
E40        2       NEISSERIA MENINGITIDIS, SEROGROUP Y --GENETICS
E41        2       NEISSERIA MENINGITIDIS, SEROGROUP Y --ISOLATIO
E42      788   19  NEISSERIACEAE
E43        8       NEISSERIACEAE --ANALYSIS --AN
E44        3       NEISSERIACEAE --CHEMISTRY --CH
E45       46       NEISSERIACEAE --CLASSIFICATION --CL
E46        1       NEISSERIACEAE --CYTOLOGY --CY
E47       58       NEISSERIACEAE --DRUG EFFECTS --DE
E48       45       NEISSERIACEAE --ENZYMOLOGY --EN

          Enter P or PAGE for more
?p

Ref    Items  Index-term
E49       21  NEISSERIACEAE --GENETICS --GE
E50       10  NEISSERIACEAE --GROWTH AND DEVELOPMENT --GD
?s e1-e50
          1307  NEISSERIA MENINGITIDIS --ISOLATION AND PURIFIC
           310  NEISSERIA MENINGITIDIS --METABOLISM --ME
           348  NEISSERIA MENINGITIDIS --PATHOGENICITY --PY
           109  NEISSERIA MENINGITIDIS --PHYSIOLOGY --PH
             3  NEISSERIA MENINGITIDIS --RADIATION EFFECTS --R
            90  NEISSERIA MENINGITIDIS --ULTRASTRUCTURE --UL
             4  NEISSERIA MENINGITIDIS --VIROLOGY --VI
             9  NEISSERIA MENINGITIDIS, SEROGROUP A
             1  NEISSERIA MENINGITIDIS, SEROGROUP A --CLASSIFI
             2  NEISSERIA MENINGITIDIS, SEROGROUP A --GENETICS
             7  NEISSERIA MENINGITIDIS, SEROGROUP A --IMMUNOLO
             2  NEISSERIA MENINGITIDIS, SEROGROUP A --ISOLATIO
             1  NEISSERIA MENINGITIDIS, SEROGROUP A --PATHOGEN
            21  NEISSERIA MENINGITIDIS, SEROGROUP B
             1  NEISSERIA MENINGITIDIS, SEROGROUP B --ENZYMOLO
             7  NEISSERIA MENINGITIDIS, SEROGROUP B --GENETICS
             1  NEISSERIA MENINGITIDIS, SEROGROUP B --GROWTH A
            14  NEISSERIA MENINGITIDIS, SEROGROUP B --IMMUNOLO
             4  NEISSERIA MENINGITIDIS, SEROGROUP B --ISOLATIO
             2  NEISSERIA MENINGITIDIS, SEROGROUP B --METABOLI
             6  NEISSERIA MENINGITIDIS, SEROGROUP B --PATHOGEN
            34  NEISSERIA MENINGITIDIS, SEROGROUP C
             1  NEISSERIA MENINGITIDIS, SEROGROUP C --CLASSIFI
             1  NEISSERIA MENINGITIDIS, SEROGROUP C --ENZYMOLO
             4  NEISSERIA MENINGITIDIS, SEROGROUP C --GENETICS
             1  NEISSERIA MENINGITIDIS, SEROGROUP C --GROWTH A
            15  NEISSERIA MENINGITIDIS, SEROGROUP C --IMMUNOLO
            11  NEISSERIA MENINGITIDIS, SEROGROUP C --ISOLATIO
```

```
              2  NEISSERIA MENINGITIDIS, SEROGROUP C --METABOLI
              4  NEISSERIA MENINGITIDIS, SEROGROUP C --PATHOGEN
              9  NEISSERIA MENINGITIDIS, SEROGROUP W-135
              3  NEISSERIA MENINGITIDIS, SEROGROUP W-135 --CLAS
              2  NEISSERIA MENINGITIDIS, SEROGROUP W-135 --GENE
              2  NEISSERIA MENINGITIDIS, SEROGROUP W-135 --IMMU
              6  NEISSERIA MENINGITIDIS, SEROGROUP W-135 --ISOL
              4  NEISSERIA MENINGITIDIS, SEROGROUP Y
              2  NEISSERIA MENINGITIDIS, SEROGROUP Y --CLASSIFI
              1  NEISSERIA MENINGITIDIS, SEROGROUP Y --DRUG EFF
              1  NEISSERIA MENINGITIDIS, SEROGROUP Y --ENZYMOLO
              2  NEISSERIA MENINGITIDIS, SEROGROUP Y --GENETICS
              2  NEISSERIA MENINGITIDIS, SEROGROUP Y --ISOLATIO
            788  NEISSERIACEAE
              8  NEISSERIACEAE --ANALYSIS --AN
              3  NEISSERIACEAE --CHEMISTRY --CH
             46  NEISSERIACEAE --CLASSIFICATION --CL
              1  NEISSERIACEAE --CYTOLOGY --CY
             58  NEISSERIACEAE --DRUG EFFECTS --DE
             45  NEISSERIACEAE --ENZYMOLOGY --EN
             21  NEISSERIACEAE --GENETICS --GE
             10  NEISSERIACEAE --GROWTH AND DEVELOPMENT --GD
      S6    2796  E1-E50
?ds

Set     Items   Description
S1      10402   'SERINE PROTEASES' OR 'SERINE ENDOPEPTIDASES'
S2      37019   R1-R5
S3        332   'ENTEROPEPTIDASE'
S4      14699   E3-E12
S5      11239   E13-E50
S6       2796   E1-E50
?s (s1 or s2 or s3) and (s4 or s5 or s6)
          10402  S1
          37019  S2
            332  S3
          14699  S4
          11239  S5
           2796  S6
      S7      76  (S1 OR S2 OR S3) AND (S4 OR S5 OR S6)
?s s7/1997:2003
             76  S7
        3305438  PY=1997 : PY=2003
      S8      43  S7/1997:2003
?s s7 not s8
             76  S7
             43  S8
      S9      33  S7 NOT S8
?t s9/9/all

 9/9/1
DIALOG(R)File 155:MEDLINE(R)
(c) format only 2003 The Dialog Corp. All rts. reserv.

10797128   97086622   PMID: 8932311
  Characterization of EspC, a 110-kilodalton protein secreted by
enteropathogenic Escherichia coli which is homologous to members of the
immunoglobulin A protease-like family of secreted proteins.
  Stein M; Kenny B; Stein M A; Finlay B B
  Department of Biochemistry and Molecular Biology, University of British
Columbia, Vancouver, Canada.
  Journal of bacteriology (UNITED STATES)  Nov 1996,  178  (22)  p6546-54,
ISSN 0021-9193   Journal Code: 2985120R
  Document type: Journal Article
  Languages: ENGLISH
  Main Citation Owner: NLM
  Record type: Completed
  Subfile:  INDEX MEDICUS
  Enteropathogenic Escherichia coli (EPEC) secretes at least five proteins.
```

Two of these proteins, EspA and EspB (previously called EaeB), activate signal transduction pathways in host epithelial cells. While the role of the other three proteins (39, 40, and 110 kDa) remains undetermined, secretion of all five proteins is under the control of perA, a known positive regulator of several EPEC virulence factors. On the basis of amino-terminal protein sequence data, we cloned and sequenced the gene which encodes the 110-kDa secreted protein and examined its possible role in EPEC signaling and interaction with epithelial cells. In accordance with the terminology used for espA and espB, we called this gene espC, for EPEC-secreted protein C. We found significant homology between the predicted EspC protein sequence and a family of immunoglobulin A (IgA) protease-like proteins which are widespread among pathogenic bacteria. Members of this protein family are found in avian pathogenic Escherichia coli (Tsh), Haemophilus influenzae (Hap), and Shigella flexneri (SepA). Although these proteins and EspC do not encode IgA protease activity, they have considerable homology with IgA protease from **Neisseria** gonorrhoeae and H. influenzae and appear to use a export system for secretion. We found that genes homologous to espC also exist in other pathogenic bacteria which cause attaching and effacing lesions, including Hafnia alvei biotype 19982, Citrobacter freundii biotype 4280, and rabbit diarrheagenic E. coli (RDEC-1). Although these strains secrete various proteins similar in molecular size to the proteins secreted by EPEC, we did not detect secretion of a 110-kDa protein by these strains. To examine the possible role of EspC in EPEC interactions with epithelial cells, we constructed a deletion mutant in espC by allelic exchange and characterized the mutant by standard tissue culture assays. We found that EspC is not necessary for mediating EPEC-induced signal transduction in HeLa epithelial cells and does not play a role in adherence or invasion of tissue culture cells.

Tags: Comparative Study; Human; Support, Non-U.S. Gov't

Descriptors: *Bacterial Proteins--secretion--SE; *Escherichia coli --genetics--GE; *Escherichia coli--pathogenicity--PY; *Genes, Structural, Bacterial; *Intestines--microbiology--MI; Amino Acid Sequence; Bacterial Proteins--genetics--GE; Bacterial Proteins--metabolism--ME; Caco-2 Cells; Cell Communication; Chromosomes, Bacterial; Cloning, Molecular; Databases, Factual; Enterobacteriaceae--genetics--GE; Enterobacteriaceae--pathogenicity--PY; Epithelium--microbiology--MI; Epithelium--pathology--PA; Escherichia coli--enzymology--EN; Hela Cells; Molecular Sequence Data; Mutation; Sequence Analysis, DNA; Sequence Homology, Amino Acid; **Serine Endopeptidases --genetics** --GE; Species Specificity

Molecular Sequence Databank No.: GENBANK/U69128

CAS Registry No.: 0 (Bacterial Proteins); 0 (EspC protein)

Enzyme No.: EC 3.4.21 (Serine **Endopeptidases**); EC 3.4.21.72 (IgA-specific serine endopeptidase)

Record Date Created: 19970107

Record Date Completed: 19970107

9/9/2

DIALOG(R)File 155:MEDLINE(R)

10791088 97080554 PMID: 8921899

Absence of periplasmic DsbA oxidoreductase facilitates export of cysteine-containing passenger proteins to the Escherichia coli cell surface via the Iga beta autotransporter pathway.

Jose J; Kramer J; Klauser T; Pohlner J; Meyer T F

Max-Planck-Institut fur Biologie, Abteilung Infektionsbiologie, Tubingen, Germany.

Gene (NETHERLANDS) Oct 31 1996, 178 (1-2) p107-10, ISSN 0378-1119 Journal Code: 7706761

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

The Iga beta autotransporter function of IgA1 protease from **Neisseria** gonorrhoeae was assessed in Escherichia coli using the Vibrio cholerae toxin B subunit (CtxB) as a heterologous passenger. N-terminal fusions with Iga beta of native CtxB or mutant CtxB protein containing no cysteines were

constructed and analysed in isogenic E. coli mutants carrying defects in either or both the ompT (outer membrane protease T) and dsbA (periplasmic disulfide oxidoreductase) determinants. While export of the cystein-less CtxB passenger was independent of the dsbA genotype, the native CtxB passenger was properly translocated across the outer membrane only in the dsbA mutant background. This effect was consistent in the presence and in the absence of the OmpT protease which rather determined the release of surface-bound CtxB into the medium. Therefore, in agreement with previous observations Iga beta-dependent protein secretion requires an unfolded conformation of the passenger domain and can be blocked by disulfide loop formation in the presence of DsbA. Since DsbA acts in the periplasm, this provides evidence for a periplasmic intermediate in the Iga beta-mediated export pathway. E. coli (dsbA ompT) is highly suitable as a strain for the surface display of recombinant proteins via Iga beta, whether or not they contain cysteine residues.

Tags: Support, Non-U.S. Gov't

Descriptors: Cysteine--metabolism--ME; *Escherichia coli--metabolism--ME; *Isomerases--metabolism--ME; *Oxidoreductases--metabolism--ME; * **Serine Endopeptidases --metabolism** --ME; Biological Transport; Cell Membrane --metabolism--ME; Cholera Toxin--genetics--GE; Cholera Toxin--metabolism --ME; Escherichia coli--enzymology--EN; Escherichia coli--genetics--GE; Isomerases--genetics--GE; Molecular Sequence Data; Mutation; Oxidoreductases--genetics--GE; Protein Disulfide-Isomerase; Recombinant Fusion Proteins--genetics--GE; Recombinant Fusion Proteins--metabolism--ME ; Recombinant Fusion Proteins--secretion--SE; **Serine Endopeptidases --genetics** --GE; Vibrio cholerae--genetics--GE

Molecular Sequence Databank No.: GENBANK/X80762

CAS Registry No.: 0 (Recombinant Fusion Proteins); 52-90-4 (Cysteine) ; 9012-63-9 (Cholera Toxin)

Enzyme No.: EC 1. (Oxidoreductases); EC 1.8.4.- (periplasmic protein disulfide oxidoreductase); EC 3.4.21 (Serine **Endopeptidases**); EC 3.4.21.72 (IgA-specific serine endopeptidase); EC 3.4.21.87 (omptin); EC 5. (Isomerases); EC 5.3.4.1 (Protein Disulfide-Isomerase)

Record Date Created: 19961231

Record Date Completed: 19961231

9/9/3

DIALOG(R)File 155:MEDLINE(R)

10737128 97086622 PMID: 8932311

Characterization of EspC, a 110-kilodalton protein secreted by enteropathogenic Escherichia coli which is homologous to members of the immunoglobulin A protease-like family of secreted proteins.

Stein M; Kenny B; Stein M A; Finlay B B

Department of Biochemistry and Molecular Biology, University of British Columbia, Vancouver, Canada.

Journal of bacteriology (UNITED STATES) Nov 1996, 178 (22) p6546-54, ISSN 0021-9193 Journal Code: 2985120R

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

Enteropathogenic Escherichia coli (EPEC) secretes at least five proteins. Two of these proteins, EspA and EspB (previously called EaeB), activate signal transduction pathways in host epithelial cells. While the role of the other three proteins (39, 40, and 110 kDa) remains undetermined, secretion of all five proteins is under the control of perA, a known positive regulator of several EPEC virulence factors. On the basis of amino-terminal protein sequence data, we cloned and sequenced the gene which encodes the 110-kDa secreted protein and examined its possible role in EPEC signaling and interaction with epithelial cells. In accordance with the terminology used for espA and espB, we called this gene espC, for EPEC-secreted protein C. We found significant homology between the predicted EspC protein sequence and a family of immunoglobulin A (IgA) protease-like proteins which are widespread among pathogenic bacteria. Members of this protein family are found in avian pathogenic Escherichia

coli (Tsh), Haemophilus influenzae (Hap), and Shigella flexneri (SepA). Although these proteins and EspC do not encode IgA protease activity, they have considerable homology with IgA protease from **Neisseria** gonorrhoeae and H. influenzae and appear to use a export system for secretion. We found that genes homologous to espC also exist in other pathogenic bacteria which cause attaching and effacing lesions, including Hafnia alvei biotype 19982, Citrobacter freundii biotype 4280, and rabbit diarrheagenic E. coli (RDEC-1). Although these strains secrete various proteins similar in molecular size to the proteins secreted by EPEC, we did not detect secretion of a 110-kDa protein by these strains. To examine the possible role of EspC in EPEC interactions with epithelial cells, we constructed a deletion mutant in espC by allelic exchange and characterized the mutant by standard tissue culture assays. We found that EspC is not necessary for mediating EPEC-induced signal transduction in HeLa epithelial cells and does not play a role in adherence or invasion of tissue culture cells.

Tags: Comparative Study; Human; Support, Non-U.S. Gov't

Descriptors: *Bacterial Proteins--secretion--SE; *Escherichia coli --genetics--GE; *Escherichia coli--pathogenicity--PY; *Genes, Structural, Bacterial; *Intestines--microbiology--MI; Amino Acid Sequence; Bacterial Proteins--genetics--GE; Bacterial Proteins--metabolism--ME; Caco-2 Cells; Cell Communication; Chromosomes, Bacterial; Cloning, Molecular; Databases, Factual; Enterobacteriaceae--genetics--GE; Enterobacteriaceae--pathogenicity--PY; Epithelium--microbiology--MI; Epithelium--pathology--PA; Escherichia coli--enzymology--EN; Hela Cells; Molecular Sequence Data; Mutation; Sequence Analysis, DNA; Sequence Homology, Amino Acid; **Serine Endopeptidases --genetics** --GE; Species Specificity

Molecular Sequence Databank No.: GENBANK/U69128

CAS Registry No.: 0 (Bacterial Proteins); 0 (EspC protein)

Enzyme No.: EC 3.4.21 (Serine **Endopeptidases**); EC 3.4.21.72 (IgA-specific serine endopeptidase)

Record Date Created: 19970107

Record Date Completed: 19970107

9/9/4

DIALOG(R)File 155:MEDLINE(R)

10731088 97080554 PMID: 8921899

Absence of periplasmic DsbA oxidoreductase facilitates export of cysteine-containing passenger proteins to the Escherichia coli cell surface via the Iga beta autotransporter pathway.

Jose J; Kramer J; Klauser T; Pohlner J; Meyer T F

Max-Planck-Institut fur Biologie, Abteilung Infektionsbiologie, Tubingen, Germany.

Gene (NETHERLANDS) Oct 31 1996, 178 (1-2) p107-10, ISSN 0378-1119 Journal Code: 7706761

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

The Iga beta autotransporter function of IgA1 protease from **Neisseria** gonorrhoeae was assessed in Escherichia coli using the Vibrio cholerae toxin B subunit (CtxB) as a heterologous passenger. N-terminal fusions with Iga beta of native CtxB or mutant CtxB protein containing no cysteines were constructed and analysed in isogenic E. coli mutants carrying defects in either or both the ompT (outer membrane protease T) and dsbA (periplasmic disulfide oxidoreductase) determinants. While export of the cystein-less CtxB passenger was independent of the dsbA genotype, the native CtxB passenger was properly translocated across the outer membrane only in the dsbA mutant background. This effect was consistent in the presence and in the absence of the OmpT protease which rather determined the release of surface-bound CtxB into the medium. Therefore, in agreement with previous observations Iga beta-dependent protein secretion requires an unfolded conformation of the passenger domain and can be blocked by disulfide loop formation in the presence of DsbA. Since DsbA acts in the periplasm, this provides evidence for a periplasmic intermediate in the Iga beta-mediated export pathway. E. coli (dsbA ompT) is highly suitable as a strain for the

surface display of recombinant proteins via Iga beta, whether or not they contain cysteine residues.
Tags: Support, Non-U.S. Gov't
Descriptors: Cysteine--metabolism--ME; *Escherichia coli--metabolism--ME; *Isomerases--metabolism--ME; *Oxidoreductases--metabolism--ME; * **Serine Endopeptidases --metabolism** --ME; Biological Transport; Cell Membrane --metabolism--ME; Cholera Toxin--genetics--GE; Cholera Toxin--metabolism --ME; Escherichia coli--enzymology--EN; Escherichia coli--genetics--GE; Isomerases--genetics--GE; Molecular Sequence Data; Mutation; Oxidoreductases--genetics--GE; Protein Disulfide-Isomerase; Recombinant Fusion Proteins--genetics--GE; Recombinant Fusion Proteins--metabolism--ME ; Recombinant Fusion Proteins--secretion--SE; **Serine Endopeptidases --genetics** --GE; Vibrio cholerae--genetics--GE
Molecular Sequence Databank No.: GENBANK/X80762
CAS Registry No.: 0 (Recombinant Fusion Proteins); 52-90-4 (Cysteine) ; 9012-63-9 (Cholera Toxin)
Enzyme No.: EC 1. (Oxidoreductases); EC 1.8.4.- (periplasmic protein disulfide oxidoreductase); EC 3.4.21 (Serine **Endopeptidases**); EC 3.4.21.72 (IgA-specific serine endopeptidase); EC 3.4.21.87 (omptin); EC 5. (Isomerases); EC 5.3.4.1 (Protein Disulfide-Isomerase)
Record Date Created: 19961231
Record Date Completed: 19961231

9/9/5
DIALOG(R)File 155:MEDLINE(R)

10706086 97055419 PMID: 8899706
Processing of the AIDA-I precursor: removal of AIDAc and evidence for the outer membrane anchoring as a beta-barrel structure.
Suhr M; Benz I; Schmidt M A
Institut fur Infektiologie, Zentrum fur Molekularbiologie, Entzundung (ZMBE), Munster, Germany.
Molecular microbiology (ENGLAND) Oct 1996, 22 (1) p31-42, ISSN 0950-382X Journal Code: 8712028
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Subfile: INDEX MEDICUS
The AIDA-I adhesin known to be responsible for the diffuse adherence (DA) phenotype of the diarrhoeagenic Escherichia coli (DAEC) strain 2787 has been shown previously to be synthesized as a precursor protein and to undergo additional C-terminal processing. Here, the C-terminal processing of the AIDA-I precursor and the outer membrane topology of the cleaved C-terminal fragment, AIDAc, were investigated. By isolation of the cleaved AIDAc fragment and N-terminal sequencing, the C-terminal cleavage site was identified between Ser-846 and Ala-847 thereby indicating a molecular mass of 47.5 kDa for AIDAc. The correct processing to AIDA-I and AIDAc in OmpT, OmpP and DegP protease-deficient E. coli strains as well as in avirulent salmonellae and shigellae points to an autocatalytic cleavage mechanism. The cleaved AIDAc was localized in the outer membrane. A leader sequence-AIDAc fusion was efficiently routed to the outer membrane. Analysis by protease digestion, secondary-structure prediction and modelling, by comparison with structurally related bacterial proteins like the IgA1 protease from **neisseria** , the vacuolating toxin from Helicobacter pylori, and the VirG protein of Shigella flexneri, strongly indicates that AIDAc is present in the outer membrane as a beta-barrel structure.
Descriptors: *Adhesins, Escherichia coli--biosynthesis--BI; *Escherichia coli--metabolism--ME; *Protein Precursors--metabolism--ME; *Protein Processing, Post-Translational; *Protein Structure, Secondary; Adhesins, Escherichia coli--chemistry--CH; Adhesins, Escherichia coli--immunology --IM; Amino Acid Sequence; Antibodies, Bacterial; Blotting, Western; Cell Compartmentation; Cell Membrane--ultrastructure--UL; **Endopeptidases** --deficiency--DF; **Endopeptidases** --metabolism--ME; Escherichia coli --genetics--GE; Molecular Sequence Data; Protein Precursors--chemistry--CH; Protein Precursors--immunology--IM; Sequence Analysis
Molecular Sequence Databank No.: GENBANK/X65022

CAS Registry No.: 0 (AIDA-I protein); 0 (Adhesins, Escherichia coli); 0 (Antibodies, Bacterial); 0 (Protein Precursors)
Enzyme No.: EC 3.4.- (**Endopeptidases**)
Record Date Created: 19970219
Record Date Completed: 19970219

9/9/6
DIALOG(R)File 155:MEDLINE(R)

10600311 96417863 PMID: 8820654
Cloning of an Aeromonas hydrophila type IV pilus biogenesis gene cluster: complementation of pilus assembly functions and characterization of a type IV leader peptidase/N-methyltransferase required for extracellular protein secretion.
Pepe C M; Eklund M W; Strom M S
US Department of Commerce, NOAA, Seattle, Washington 98112-2097, USA.
Molecular microbiology (ENGLAND) Feb 1996, 19 (4) p857-69, ISSN 0950-382X Journal Code: 8712028
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Subfile: INDEX MEDICUS
Aeromonas hydrophila secretes several extracellular proteins that are associated with virulence including an enterotoxin, a protease, and the hole-forming toxin, aerolysin. These degradative enzymes and toxins are exported by a conserved pathway found in many Gram-negative bacteria. In Pseudomonas aeruginosa this export pathway and type IV pilus biogenesis are dependent on the product of the pilD gene. PilD is a bifunctional enzyme that processes components of the extracellular secretory pathway as well as a type IV prepilin. An A. hydrophila genomic library was transferred into a P. aeruginosa pilD mutant that is defective for type IV pilus biogenesis. The A. hydrophila pilD homologue, tapD, was identified by its ability to complement the pilD mutation in P. aeruginosa. Transconjugants containing tapD were sensitive to the type IV pilus-specific phage, PO4. Sequence data revealed that tapD is part of a cluster of genes (tapABCD) that are homologous to P. aeruginosa type IV pilus biogenesis genes (pilABCD). We showed that TapB and TapC are functionally homologous to P. aeruginosa PilB and PilC, the first such functional complementation of pilus assembly demonstrated between bacteria that express type IV pili. In vitro studies revealed that TapD has both endopeptidase and N-methyltransferase activities using P. aeruginosa prepilin as substrate. Furthermore, we show that tapD is required for extracellular secretion of aerolysin and protease, indicating that tapD may play an important role in the virulence of A. hydrophila.
Tags: Support, U.S. Gov't, Non-P.H.S.
Descriptors: Aeromonas hydrophila--genetics--GE; *Bacterial Proteins --secretion--SE; * **Endopeptidases** --genetics--GE; *Fimbriae, Bacterial --genetics--GE; *Genes, Bacterial; *Methyltransferases--genetics--GE; *Multienzyme Complexes--genetics--GE; Amino Acid Sequence; Bacterial Proteins--genetics--GE; Bacterial Toxins--metabolism--ME; Base Sequence; Cloning, Molecular; Genetic Complementation Test; Molecular Sequence Data; Multigene Family; Mutation; Sequence Analysis, DNA; Sequence Homology, Amino Acid
Molecular Sequence Databank No.: GENBANK/U20255
CAS Registry No.: 0 (Bacterial Proteins); 0 (Bacterial Toxins); 0 (Multienzyme Complexes); 0 (PilD protein); 0 (pilC protein, Neisseria gonorrhoeae); 122319-68-0 (pilB protein); 53126-24-2 (aerolysin)
Enzyme No.: EC 2.1.1. (Methyltransferases); EC 3.4.- (**Endopeptidases**); EC 3.4.99.- (TapD protein)
Record Date Created: 19961216
Record Date Completed: 19961216

9/9/7
DIALOG(R)File 155:MEDLINE(R)

10491810 96302316 PMID: 8703438

Biological significance of IgA1 proteases in bacterial colonization and pathogenesis: critical evaluation of experimental evidence.

Kilian M; Reinholdt J; Lomholt H; Poulsen K; Frandsen E V

Department of Medical Microbiology and Immunology, Faculty of Health Sciences, University of Aarhus, Denmark.

APMIS - acta pathologica, microbiologica, et immunologica Scandinavica (DENMARK) May 1996, 104 (5) p321-38, ISSN 0903-4641 Journal Code: 8803400

Document type: Journal Article; Review; Review, Tutorial

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

IgA1 protease activity, which allows bacteria to cleave human IgA1 in the hinge region, represents a striking example of convergent evolution of a specific property in bacteria. Although it has been known since 1979 that IgA1 protease is produced by the three leading causes of bacterial meningitis in addition to important urogenital pathogens and some members of the oropharyngeal flora, the exact role of this enzyme in bacterial pathogenesis is still incompletely understood owing to lack of a satisfactory animal model. Cleavage of IgA1 by these post-proline **endopeptidases** efficiently separates the monomeric antigen-binding fragments from the secondary effector functions of the IgA1 antibody molecule. Several in vivo and in vitro observations indicate that the enzymes are important for the ability of bacteria to colonize mucosal membranes in the presence of S-IgA antibodies. Furthermore, the extensive cleavage of IgA sometimes observed in vivo, suggests that IgA1 protease activity results in a local functional IgA deficiency that may facilitate colonization of other microorganisms and the penetration of potential allergens. It has been hypothesized that IgA1 protease activity of Haemophilus influenzae, **Neisseria** meningitidis, and Streptococcus pneumoniae, under special immunological circumstances, allows these bacteria to take advantage of specific IgA1 antibodies in a strategy to evade other immune factors of the human body. The decisive factor is the balance between IgA antibodies against surface antigens of the respective bacteria and their IgA1 protease. Recent studies have shown that serine-type IgA1 proteases of H. influenzae, meningococci, and gonococci belong to a family of proteins used by a diverse group of Gram-negative bacteria for colonization and invasion. (155 Refs.)

Tags: Animal; Human

Descriptors: Bacteria--enzymology--EN; *Bacteria--pathogenicity--PY; *Bacterial Infections--enzymology--EN; *Bacterial Infections--microbiology --MI; *Immunoglobulin A--physiology--PH; * **Serine Endopeptidases --physiology** --PH; Amino Acid Sequence; Bacteria--immunology--IM; Bacterial Infections--immunology--IM; Molecular Sequence Data; Virulence

CAS Registry No.: 0 (Immunoglobulin A)

Enzyme No.: EC 3.4.21 (Serine **Endopeptidases**); EC 3.4.21.72 (IgA-specific serine endopeptidase)

Record Date Created: 19960909

Record Date Completed: 19960909

9/9/8

DIALOG(R)File 155:MEDLINE(R)

10449888 96256608 PMID: 8655552

The cryptic general secretory pathway (gsp) operon of Escherichia coli K-12 encodes functional proteins.

Francetic O; Pugsley A P

Unite de Genetique Moleculaire, Centre National de la Recherche Scientifique Unite de Recherche Associee 1149, Institut Pasteur, Paris, France.

Journal of bacteriology (UNITED STATES) Jun 1996, 178 (12) p3544-9, ISSN 0021-9193 Journal Code: 2985120R

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM
Record type: Completed
Subfile: INDEX MEDICUS

Systematic sequencing of the Escherichia coli K-12 chromosome (GenBank entry U18997) has revealed the presence of an apparently complete operon of genes (the gspC-0 operon) similar to genes coding for components of the main terminal branch of the general secretory pathway (e.g., the Klebsiella oxytoca pulC-0 pullulanase secretion operon) and to related genes required for type IV pilus biogenesis. For example, the last gene in the gsp operon, gspO (formerly hopD), encodes a protein which is similar to several type IV prepilin peptidases. Expression of gspO from lacZp promotes cleavage of two known prepilin peptidase substrates in E. coli K-12: **Neisseria** gonorrhoeae type IV prepilin and K. oxytoca prePulG protein. gspO also complements a mutation in the corresponding gene (pulO) of the pullulanase secretion operon when it is expressed from lacZp. Another gene in the gsp operon, gspG (formerly hopG), encodes a protein similar to prePulG, a component of the pullulanase secretion pathway. Expression of gspG from lacZp leads to production of a protein which (i) is recognized by PulG-specific antiserum (and by antiserum against the Pseudomonas aeruginosa PulG homolog XcpG [formerly XcpT]), (ii) is processed in cells expressing gspO, and (iii) restores secretion in cells carrying a pulG mutation. The chromosomal copies of gspG and gspO are apparently not expressed, probably because of very weak transcription from the upstream region, as measured by using a chromosomal gspC-lacZ operon fusion. Thus, the gsp operon of E. coli K-12 includes at least two functional genes which, together with the rest of the operon, are probably not expressed under laboratory conditions.

Tags: Support, Non-U.S. Gov't

Descriptors: *Bacterial Proteins--genetics--GE; *Bacterial Proteins --secretion--SE; *Escherichia coli--genetics--GE; Bacterial Outer Membrane Proteins--metabolism--ME; Base Sequence; DNA, Bacterial--genetics--GE; **Endopeptidases** --genetics--GE; Fimbriae Proteins; Gene Expression Regulation, Bacterial; Genes, Structural, Bacterial; Genetic Complementation Test; Glycoside Hydrolases--genetics--GE; Molecular Sequence Data; Operon; Promoter Regions (Genetics); RNA, Messenger --genetics--GE; Regulatory Sequences, Nucleic Acid; Transcription, Genetic

Molecular Sequence Databank No.: GENBANK/U18997

CAS Registry No.: 0 (Bacterial Outer Membrane Proteins); 0 (Bacterial Proteins); 0 (DNA, Bacterial); 0 (RNA, Messenger); 147680-16-8 (Fimbriae Proteins)

Enzyme No.: EC 3.2.1. (Glycoside Hydrolases); EC 3.2.1.41 (pullulanase); EC 3.4.- (**Endopeptidases**)

Record Date Created: 19960730

Record Date Completed: 19960730

9/9/9

DIALOG(R)File 155:MEDLINE(R)

10381215 96186495 PMID: 8641803

Analysis of the specificity of bacterial immunoglobulin A (IgA) proteases by a comparative study of ape serum IgAs as substrates.

Qiu J; Brackee G P; Plaut A G

Gastroenterology Division, Department of Medicine, Tufts-New England Medical Center, Boston, Massachusetts 02111, USA.

Infection and immunity (UNITED STATES) Mar 1996, 64 (3) p933-7, ISSN 0019-9567 Journal Code: 0246127

Contract/Grant No.: NIDR-DE 06977; DE; NIDCR

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

Immunoglobulin A (IgA) proteases are bacterial enzymes with substrate specificity for human serum and secretory IgAs. To further define the basis of this specificity, we examined the ability of IgA proteases of Clostridium ramosum, Streptococcus pneumoniae (EC 3.4.24.13), **Neisseria** meningitidis (EC 3.4.21.72), and Haemophilus influenzae (EC 3.4.21.72) to

Institute of Medical Microbiology, University of Aarhus, Denmark.
Vaccine (ENGLAND) Sep 1995, 13 (13) p1213-9, ISSN 0264-410X Journal Code: 8406899
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Subfile: INDEX MEDICUS

The antigenic diversity among IgA1 proteases of 61 **Neisseria** gonorrhoeae strains isolated during a period of 23 years and on four continents was examined in enzyme neutralization assays employing rabbit antisera raised against selected IgA1 proteases. The antigenic analyses were compared with results of iga gene-region RFLP patterns and enzyme cleavage specificity for substrate IgA1. Type 1 IgA1 proteases were antigenically uniform while six different antigenic types were detected among type 2 enzymes. Extensive cross-reactions of antibodies against the different antigenic types suggested only minor differences in relevant epitopes. Epitopes previously found to be common to all **Neisseria** meningitidis IgA1 proteases were also shared by all N. gonorrhoeae IgA1 proteases in the collection. Human sera from patients with gonorrhoea showed broadly cross-reactive neutralizing activity at titers comparable to those of sera from immunized rabbits. In conclusion, N. gonorrhoeae IgA1 proteases show a remarkable lack of diversity of epitopes recognized by enzyme-neutralizing antibodies. If future studies confirm that cleavage of IgA1 is an important step in gonococcal infections, **Neisseria** IgA1 proteases may be attractive vaccine candidates.

Tags: Animal; Comparative Study; Human; Support, Non-U.S. Gov't
Descriptors: Cross Reactions; *Epitope Mapping; * **Neisseria** gonorrhoeae --physiology--PH; * **Serine Endopeptidases --immunology** --IM; Epitopes; Genes, Bacterial; Immunoglobulin A--genetics--GE; **Neisseria** gonorrhoeae --enzymology--EN; **Neisseria** gonorrhoeae--immunology--IM; Neutralization Tests; Polymorphism, Restriction Fragment Length; Rabbits; Serotyping; Substrate Specificity
CAS Registry No.: 0 (Epitopes); 0 (Immunoglobulin A)
Enzyme No.: EC 3.4.21 (Serine **Endopeptidases**); EC 3.4.21.72 (IgA-specific serine endopeptidase)
Record Date Created: 19960308
Record Date Completed: 19960308

9/9/13
DIALOG(R)File 155:MEDLINE(R)

10222271 96023519 PMID: 7548543
Comparative studies of the IgA1 protease genes from Haemophilus influenzae, Neisseria **gonorrhoeae, and Prevotella melaninogenica.**
Arzese A; Botta G A
Institute of Microbiology, School of Medicine, University of Udine, Italy.
Clinical infectious diseases - an official publication of the Infectious Diseases Society of America (UNITED STATES) Jun 1995, 20 Suppl 2 pS169-71, ISSN 1058-4838 Journal Code: 9203213
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Subfile: INDEX MEDICUS
Tags: Comparative Study; Human; Support, Non-U.S. Gov't
Descriptors: Haemophilus influenzae--enzymology--EN; * **Neisseria** gonorrhoeae--enzymology--EN; *Prevotella--enzymology--EN; * **Serine Endopeptidases --genetics** --GE; Genes, Bacterial; Haemophilus influenzae --genetics--GE; Immunoglobulin A; **Neisseria** gonorrhoeae--genetics--GE; Prevotella--genetics--GE
CAS Registry No.: 0 (Immunoglobulin A)
Enzyme No.: EC 3.4.21 (Serine **Endopeptidases**); EC 3.4.21.72 (IgA-specific serine endopeptidase)
Gene Symbol: iga
Record Date Created: 19951102

Record Date Completed: 19951102

9/9/14
DIALOG(R)File 155:MEDLINE(R)

10219448 96020667 PMID: 7476198
SepA, the major extracellular protein of Shigella flexneri: autonomous secretion and involvement in tissue invasion.
Benjelloun-Touimi Z; Sansonetti P J; Parsot C
Unite de Pathogenie Microbienne Moleculaire, INSERM U389, Institut Pasteur, Paris, France.
Molecular microbiology (ENGLAND) Jul 1995, 17 (1) p123-35, ISSN 0950-382X Journal Code: 8712028
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Subfile: INDEX MEDICUS
In addition to Ipa proteins and IcsA, which are involved in entry into epithelial cells and intercellular spread, respectively, Shigella secretes a 110 kDa protein, designated SepA. We report the identification, cloning, and nucleotide sequence determination of the sepA gene, analysis of SepA secretion, and construction and characterization of a sepA mutant. The sepA gene is carried by the virulence plasmid and codes for a 150 kDa precursor. Upon secretion, which does not involve accessory proteins encoded by the virulence plasmid, the precursor is converted to a mature protein of 110 kDa by two cleavages removing an N-terminal signal sequence and a C-terminal fragment. Extensive similarities were detected between the sequence of the first 500 residues of mature SepA and the N-terminal region of IgA1 proteases from **Neisseria** gonorrhoeae and Haemophilus influenzae, the Tsh haemagglutinin of an avian pathogenic Escherichia coli, and the Hap protein involved in adhesion and penetration of H. influenzae. The C-terminal domain of the SepA precursor, which is not present in the secreted protein, exhibits sequence similarity with pertactin of Bordetella pertussis and the ring-forming protein of Helicobacter mustelae. Construction and phenotypic characterization of a sepA mutant indicated that SepA is required neither for entry into cultured epithelial cells nor for intercellular dissemination. However, in the rabbit ligated ileal loop model, the sepA mutant exhibited an attenuated virulence, which suggests that SepA might play a role in tissue invasion.
Tags: Animal; Support, Non-U.S. Gov't
Descriptors: *Bacterial Proteins--physiology--PH; *Bacterial Proteins --secretion--SE; *Genes, Structural, Bacterial--genetics--GE; *Shigella flexneri--pathogenicity--PY; Amino Acid Sequence; Bacterial Proteins --genetics--GE; Cloning, Molecular; Ileum--microbiology--MI; Immunoglobulin A--metabolism--ME; Molecular Sequence Data; Mucous Membrane--microbiology --MI; Mutation; Plasmids--genetics--GE; Protein Precursors--genetics--GE; Protein Processing, Post-Translational; Rabbits; Sequence Analysis; Sequence Analysis, DNA; Sequence Homology, Amino Acid; **Serine Endopeptidases --metabolism** --ME; Shigella flexneri--genetics--GE; Virulence
Molecular Sequence Databank No.: GENBANK/Z48219
CAS Registry No.: 0 (Bacterial Proteins); 0 (Immunoglobulin A); 0 (Plasmids); 0 (Protein Precursors); 0 (SepA protein, Shigella)
Enzyme No.: EC 3.4.21 (Serine **Endopeptidases**); EC 3.4.21.72 (IgA-specific serine endopeptidase)
Record Date Created: 19951218
Record Date Completed: 19951218

9/9/15
DIALOG(R)File 155:MEDLINE(R)

10200531 96001589 PMID: 8525999
Titration of inhibiting antibodies to bacterial IgA1 proteases in human sera and secretions.

Reinholdt J; Kilian M
Royal Dental College, Faculty of Health Sciences, University of Aarhus, Denmark.
Advances in experimental medicine and biology (UNITED STATES) 1995, 371A p605-8, ISSN 0065-2598 Journal Code: 0121103
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Subfile: INDEX MEDICUS
Tags: Human
Descriptors: Antibodies, Bacterial--analysis--AN; *Antigens, Bacterial --immunology--IM; *Bacterial Proteins--immunology--IM; *Colostrum --immunology--IM; *Saliva--immunology--IM; *Salivary Proteins--immunology --IM; * **Serine Endopeptidases --immunology** --IM; Antibodies, Bacterial --blood--BL; Antibodies, Bacterial--immunology--IM; Antibody Specificity; Bacterial Proteins--antagonists and inhibitors--AI; Haemophilus influenzae --immunology--IM; Immunoglobulin A, Secretory--immunology--IM; Immunoglobulin A, Secretory--isolation and purification--IP; **Neisseria** meningitidis--immunology--IM; Streptococcus--immunology--IM
CAS Registry No.: 0 (Antibodies, Bacterial); 0 (Antigens, Bacterial); 0 (Bacterial Proteins); 0 (Immunoglobulin A, Secretory); 0 (Salivary Proteins)
Enzyme No.: EC 3.4.21 (Serine **Endopeptidases**); EC 3.4.21.72 (IgA-specific serine endopeptidase)
Record Date Created: 19960124
Record Date Completed: 19960124

9/9/16
DIALOG(R)File 155:MEDLINE(R)

10200530 96001588 PMID: 8525998
Antigenic and genetic heterogeneity among Haemophilus influenzae and Neisseria IgA1 proteases.
Lomholt H; Poulsen K; Kilian M
Institute of Medical Microbiology, University of Aarhus, Denmark.
Advances in experimental medicine and biology (UNITED STATES) 1995, 371A p599-603, ISSN 0065-2598 Journal Code: 0121103
Document type: Journal Article; Review; Review, Tutorial
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Subfile: INDEX MEDICUS
(18 Refs.)
Tags: Comparative Study; Support, Non-U.S. Gov't
Descriptors: Antigens, Bacterial--genetics--GE; *Bacterial Proteins --genetics--GE; *Haemophilus influenzae--enzymology--EN; *Immunoglobulin A --metabolism--ME; * **Neisseria** --enzymology--EN; * **Serine Endopeptidases --genetics** --GE; Antigens, Bacterial--immunology--IM; Bacterial Proteins --immunology--IM; Evolution, Molecular; Genes, Structural, Bacterial; Haemophilus influenzae--genetics--GE; Haemophilus influenzae--immunology --IM; **Neisseria** --genetics--GE; **Neisseria** --immunology--IM; Phylogeny; Polymorphism, Restriction Fragment Length; **Serine Endopeptidases --immunology** --IM; Species Specificity; Substrate Specificity
CAS Registry No.: 0 (Antigens, Bacterial); 0 (Bacterial Proteins); 0 (Immunoglobulin A)
Enzyme No.: EC 3.4.21 (Serine **Endopeptidases**); EC 3.4.21.72 (IgA-specific serine endopeptidase)
Record Date Created: 19960124
Record Date Completed: 19960124

9/9/17
DIALOG(R)File 155:MEDLINE(R)

08614434 95302961 PMID: 7783620

01865495 75040397 PMID: 4214777
Studies on gonococcus infection. VI. Electron microscopic study on in vitro phagocytosis of gonococci by human leukocytes.
Swanson J ; Zeligs B
Infection and immunity (UNITED STATES) Sep **1974** , 10 (3) p645-56, ISSN 0019-9567 Journal Code: 0246127
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Subfile: INDEX MEDICUS
Tags: Human
Descriptors: Leukocytes--immunology--IM; * **Neisseria** gonorrhoeae --immunology--IM; *Phagocytosis; Histological Techniques; Leukocytes --ultrastructure--UL; Microscopy, Electron; Microscopy, Electron, Scanning; **Neisseria** gonorrhoeae--ultrastructure--UL
Record Date Created: 19750129
Record Date Completed: 19750129

3/9/2
DIALOG(R)File 155:MEDLINE(R)

01865494 75040396 PMID: 4214776
Studies on gonococcus infection. V. Observations on in vitro interactions of gonococci and human neutrophils.
Swanson J ; Sparks E; Zeligs B; Siam M A; Parrott C
Infection and immunity (UNITED STATES) Sep **1974** , 10 (3) p633-44, ISSN 0019-9567 Journal Code: 0246127
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Subfile: INDEX MEDICUS
Tags: Human
Descriptors: **Neisseria** gonorrhoeae--immunology--IM; *Neutrophils --immunology--IM; Carbon Radioisotopes; Cell Adhesion--drug effects--DE; Cell Separation; Chymotrypsin--pharmacology--PD; Glutaral--pharmacology--PD ; Heat; Hela Cells--immunology--IM; Microscopy, Electron; **Neisseria** gonorrhoeae--cytology--CY; **Neisseria** gonorrhoeae--ultrastructure--UL; Neutrophils--cytology--CY; Phagocytosis--drug effects--DE; Trypsin --pharmacology--PD
CAS Registry No.: 0 (Carbon Radioisotopes); 111-30-8 (Glutaral)
Enzyme No.: EC 3.4.21.1 (Chymotrypsin); EC 3.4.21.4 (Trypsin)
Record Date Created: 19750129
Record Date Completed: 19750129

3/9/3
DIALOG(R)File 155:MEDLINE(R)

01738316 74149824 PMID: 4207517
Differential attachment by piliated and nonpiliated Neisseria **gonorrhoeae to human sperm.**
James-Holmquest A N; **Swanson J** ; Buchanan T M; Wende R D; Williams R P
Infection and immunity (UNITED STATES) May **1974** , 9 (5) p897-902, ISSN 0019-9567 Journal Code: 0246127
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Subfile: INDEX MEDICUS
Tags: Animal; Human; In Vitro; Male
Descriptors: **Neisseria** gonorrhoeae--immunology--IM; *Spermatozoa --immunology--IM; Antibody Specificity; Bacteriological Techniques; Cell Adhesion; Cell Wall; Escherichia coli--immunology--IM; Formaldehyde; Heat; Immune Sera; Immunoglobulin G; Microscopy, Electron; Rabbits--immunology

diversity of serogroup A bacteria seems quite limited and only a few strains have been responsible for the epidemics of recent decades. Meningococci express both constant and highly variable antigens, the variability of which is determined by the clonal background of the epidemic strain. The development of an improved vaccine is being pursued but still faces technical problems. (58 Refs.)

Tags: Human

Descriptors: *Meningitis, Meningococcal--epidemiology--EP; *Neisseria meningitidis--genetics--GE; Antigens, Bacterial--immunology--IM; Disease Outbreaks; Isoenzymes--analysis--AN; Neisseria meningitidis--classification --CL; Neisseria meningitidis--immunology--IM

CAS Registry No.: 0 (Antigens, Bacterial); 0 (Isoenzymes)

Record Date Created: 19920428

Record Date Completed: 19920428

1/9/3

DIALOG(R)File 155:MEDLINE(R)

07070187 91311103 PMID: 1906911

Variation in class 5 protein expression by serogroup A meningococci during a meningitis epidemic.

Achtman M ; Wall R A; Bopp M; Kusecek B; Morelli G; Saken E; Hassan-King M

Max-Planck-Institut fur molekulare Genetik, Berlin, Germany.

Journal of infectious diseases (UNITED STATES) Aug **1991** , 164 (2) p375-82, ISSN 0022-1899 Journal Code: 0413675

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: AIM; INDEX MEDICUS

Serogroup A meningococci were isolated from patients and healthy carriers in The Gambia between 1982 and 1988. The class 5 proteins expressed by these bacteria were identified by electrophoretic migration and by serologic tests. Three protein serologic groupings (seroclasses) called A (protein 5a), B (proteins 5b, 5d, or 5e), and C (protein 5c or 5C) were found among 331 bacterial isolates. The number of class 5 proteins expressed per isolate varied from none to four, with a median of two. The class 5 protein composition differed for certain paired isolates obtained from the nasopharynx, blood, and cerebrospinal fluid of diseased patients and for certain pairs of sequential isolates from the nasopharynx of healthy carriers; the medical relevance of this variation remains unclear, although the 5C protein was preferentially isolated from the nasopharynx and the 5a protein from diseased patients. The data show that a large proportion of healthy carriers in The Gambia were exposed to bacteria expressing each of the three seroclasses and that many people were exposed to bacteria expressing each of the three seroclasses and that many people were exposed to two or all three seroclasses during the epidemic of 1982-1983.

Tags: Human; Support, Non-U.S. Gov't

Descriptors: *Disease Outbreaks; *Meningitis, Meningococcal--microbiology --MI; *Neisseria meningitidis--metabolism--ME; *Viral Proteins --biosynthesis--BI; Antibodies, Monoclonal--immunology--IM; Blotting, Western; Carrier State--microbiology--MI; Conjunctiva--microbiology--MI; Gambia--epidemiology--EP; Gene Expression Regulation, Bacterial; Meningitis, Meningococcal--blood--BL; Meningitis, Meningococcal --cerebrospinal fluid--CF; Meningitis, Meningococcal--epidemiology--EP; Nasopharynx--microbiology--MI; Neisseria meningitidis--classification--CL; Neisseria meningitidis--genetics--GE; Septicemia--microbiology--MI; Serotyping; Viral Proteins--genetics--GE

CAS Registry No.: 0 (Antibodies, Monoclonal); 0 (Viral Proteins)

Record Date Created: 19910823

Record Date Completed: 19910823

1/9/4

DIALOG(R)File 155:MEDLINE(R)

07398035 92261288 PMID: 1813777

Cloning and expression in Escherichia coli of opc, the gene for an unusual class 5 outer membrane protein from Neisseria meningitidis (meningococci/surface antigen).

Olyhoek A J; Sarkari J; Bopp M; Morelli G; **Achtman M**

Max-Planck Institut fur molekulare Genetik, Berlin, Germany.

Microbial pathogenesis (ENGLAND) Oct **1991** , 11 (4) p249-57, ISSN 0882-4010 Journal Code: 8606191

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

A genomic library was constructed in a lambda gt11 vector using chromosomal DNA from a meningococcal serogroup A strain and plaques expressing the class 5C protein were recognized by screening with specific monoclonal antibodies. The opc insert was subcloned into a multicopy plasmid which induced expression of that protein in Escherichia coli as a surface-exposed major outer membrane protein. The nucleotide sequence of opc is typical of an outer membrane protein with a promoter and terminator region, a leader peptide which is cleaved during expression and a complete open reading frame. Unlike other meningococcal class 5 proteins or gonococcal P.II proteins, the sequence did not contain any pentanucleotide repeats and the sequence showed little homology to these other functionally related proteins. However, the predicted amino acid sequence of the mature protein for opc showed 27% similarity to that for a second opa gene cloned from the same meningococcal strain. This is the first report of cloning and expression of a functional meningococcal gene encoding a class 5 outer membrane protein in E. coli.

Tags: Support, Non-U.S. Gov't

Descriptors: *Bacterial Outer Membrane Proteins--genetics--GE; *Escherichia coli--genetics--GE; *Neisseria meningitidis--genetics--GE; Amino Acid Sequence; Antibodies, Monoclonal; Antigens, Bacterial--chemistry --CH; Antigens, Bacterial--genetics--GE; Antigens, Surface--chemistry--CH; Antigens, Surface--genetics--GE; Base Sequence; Blotting, Southern; Blotting, Western; Cloning, Molecular; DNA, Bacterial--genetics--GE; Electrophoresis, Polyacrylamide Gel; Gene Expression; Genes, Bacterial; Molecular Sequence Data; Neisseria meningitidis--chemistry--CH; Neisseria meningitidis--immunology--IM; Repetitive Sequences, Nucleic Acid; Translation, Genetic

Molecular Sequence Databank No.: GENBANK/M80195; GENBANK/S72518; GENBANK/S72520; GENBANK/S78944; GENBANK/S78945; GENBANK/S78946; GENBANK/S78947; GENBANK/S78948; GENBANK/S78949; GENBANK/S78950

CAS Registry No.: 0 (Antibodies, Monoclonal); 0 (Antigens, Bacterial); 0 (Antigens, Surface); 0 (Bacterial Outer Membrane Proteins); 0 (DNA, Bacterial); 147335-96-4 (opc protein).

Record Date Created: 19920616

Record Date Completed: 19920616

1/9/2

07342709 92205828 PMID: 1803694

Clonal properties of meningococci from epidemic meningitis.

Achtman M

Max-Planck Institut fur Molekulare Genetik, Berlin, Germany.

Transactions of the Royal Society of Tropical Medicine and Hygiene (ENGLAND) **1991** , 85 Suppl 1 p24-31, ISSN 0035-9203 Journal Code: 7506129

Document type: Journal Article; Review; Review, Academic

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

Methods from the field of population genetics now enable the classification of epidemic strains of Neisseria meningitidis and have resolved the relationships between apparently distinct epidemics. The

07069402 91310318 PMID: 1677349

Virulence patterns and long-range genetic mapping of extraintestinal Escherichia coli K1, K5, and K100 isolates: use of pulsed-field gel electrophoresis.

Ott M; Bender L; Blum G; Schmittroth M; **Achtman M** ; Tschape H; Hacker J
Institut fur Genetik und Mikrobiologie, Universitat Wurzburg, Germany.

Infection and immunity (UNITED STATES) Aug **1991** , 59 (8) p2664-72, ISSN 0019-9567 Journal Code: 0246127
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Subfile: INDEX MEDICUS

A total of 127 extraintestinal Escherichia coli strains of the capsule serotypes K1, K5, and K100 from human and animal sources were analyzed for DNA sequences specific for the genes for various adhesins (P fimbriae [pap] and P-related sequences [prs], S fimbriae [sfa]/F1C fimbriae [foc], and type I fimbriae [fim]), aerobactin (aer), and hemolysin (hly). The expression of corresponding virulence factors was also tested. Twenty-four selected strains were analyzed by long-range DNA mapping to evaluate their genetic relationships. DNA sequences for the adhesins were often found in strains not expressing them, while strains with hemolysin and aerobactin genes usually did express them. Different isolates of the same serotype often expressed different virulence patterns. The use of virulence-associated gene probes for Southern hybridization with genomic DNA fragments separated by pulsed-field gel electrophoresis revealed that a highly heterogeneous restriction fragment length and hybridization pattern existed even within strains of the same serotype. Long-range DNA mapping is therefore useful for the evaluation of genetic relatedness among individual isolates and facilitates the performance of precise molecular epidemiology.

Tags: Animal; Human; Support, Non-U.S. Gov't
Descriptors: *Bacterial Proteins--genetics--GE; *Escherichia coli --genetics--GE; *Genes, Bacterial; Adhesins, Escherichia coli; Bacterial Outer Membrane Proteins--genetics--GE; Blotting, Southern; Chromosome Mapping; DNA Probes; Electrophoresis, Agar Gel; Escherichia coli --classification--CL; Escherichia coli--isolation and purification--IP; Escherichia coli--pathogenicity--PY; Fimbriae, Bacterial; Hemolysins --genetics--GE; Hydroxamic Acids--metabolism--ME; Phenotype; Polymorphism, Restriction Fragment Length; Serotyping; Virulence--genetics--GE
CAS Registry No.: 0 (Adhesins, Escherichia coli); 0 (Bacterial Outer Membrane Proteins); 0 (Bacterial Proteins); 0 (DNA Probes); 0 (Hemolysins); 0 (Hydroxamic Acids); 26198-65-2 (aerobactin)
Record Date Created: 19910823
Record Date Completed: 19910823

1/9/5

06928036 91168426 PMID: 1706236

Human hybridomas derived from CD5+ B lymphocytes of patients with chronic lymphocytic leukemia (B-CLL) produce multi-specific natural IgM (kappa) antibodies.

Jahn S; Schwab J; Hansen A; Heider H; Schroeder C; Lukowsky A; **Achtman M** ; Matthes H; Kiessig S T; Volk H D; et al
Department of Medical Immunology, Medical School (Charite), Humboldt University, Berlin, Germany.

Clinical and experimental immunology (ENGLAND) Mar **1991** , 83 (3) p413-7, ISSN 0009-9104 Journal Code: 0057202
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Subfile: INDEX MEDICUS

Great numbers of CD5+ B lymphocytes were detected in the peripheral blood of patients with B-CLL. To study the antibody repertoire of this immune

cell subpopulation on a monoclonal level, we fused the lymphocytes derived from five different donors to a highly efficient HAT-sensitive heteromyeloma line (CB-F7). A fusion frequency of up to 10(-5) allowed us to analyse hundreds of initial hybridoma lines per fusion. In all culture supernatants in three out of five fusions IgM lambda antibodies were detected, in two experiments only IgM kappa was measured, suggesting monoclonality of the primary hybridoma cell lines. The later fusions resulted in hybridomas producing multi-specific antibodies against both an autoantigen and an infectious agent: (i) dsDNA/influenza virus haemagglutinin; (ii) dsDNA/class V outer membrane protein type C from Neisseria meningitidis. However, no antibodies of the described specificity were detected in blood sera of patients, indicating a 'switch-on' of the immunoglobulin secretion capacity of malignant B cells during fusion to a myeloma partner. We discuss the results as further evidence for the natural multi-reactive antibody repertoire of CD5+ B cells.

Tags: Female; Human; Male

Descriptors: *Antigens, CD--physiology--PH; *Antigens, Differentiation --physiology--PH; *B-Lymphocytes--immunology--IM; *Immunoglobulin M --biosynthesis--BI; *Leukemia, B-Cell, Chronic--immunology--IM; Adult; Aged ; Antibodies, Monoclonal--biosynthesis--BI; Antibody Specificity; Antigens, CD5; Hybridomas--metabolism--ME; Immunoglobulins, kappa-Chain--biosynthesis --BI; Middle Age; Tumor Cells, Cultured

CAS Registry No.: 0 (Antibodies, Monoclonal); 0 (Antigens, CD); 0 (Antigens, CD5); 0 (Antigens, Differentiation); 0 (Immunoglobulin M); 0 (Immunoglobulins, kappa-Chain)

Record Date Created: 19910419

Record Date Completed: 19910419

--IM
CAS Registry No.: 0 (Immune Sera); 0 (Immunoglobulin G); 50-00-0 (Formaldehyde)
Record Date Created: 19740625
Record Date Completed: 19740625

3/9/4
DIALOG(R)File 155:MEDLINE(R)

01710172 74118041 PMID: 4205885
Gonococcal ophthalmia neonatorum. Relationship of time of infection to relevant control measures.
Thompson T R; **Swanson R E** ; Wiesner P J
JAMA - the journal of the American Medical Association (UNITED STATES) Apr 8 **1974** , 228 (2) p186-8, ISSN 0098-7484 Journal Code: 7501160
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Subfile: AIM; INDEX MEDICUS
Tags: Female; Human; Pregnancy
Descriptors: *Ophthalmia Neonatorum--etiology--ET; Adolescent; Adult; Conjunctivitis--diagnosis--DI; Eye--microbiology--MI; Fetal Diseases --diagnosis--DI; Gonorrhea--complications--CO; Infant, Newborn; Maternal-Fetal Exchange; **Neisseria** gonorrhoeae --isolation and purification--IP; Ophthalmia Neonatorum--drug therapy--DT; Ophthalmia Neonatorum--prevention and control--PC; Pregnancy Complications, Infectious ; Prenatal Diagnosis; Silver Nitrate--therapeutic use--TU
CAS Registry No.: 7761-88-8 (Silver Nitrate)
Record Date Created: 19740507
Record Date Completed: 19740507

10605582 96423170 PMID: 8825771
A physical and genetic map of Neisseria meningitidis **B1940.**
Gaher M; Einsiedler K; Crass T; Bautsch W
Institut fur Medizinische Mikrobiologie, Medizinische Hochschule Hannover, Germany.
Molecular microbiology (ENGLAND) Jan 1996, 19 (2) p249-59, ISSN 0950-382X Journal Code: 8712028
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Subfile: INDEX MEDICUS
A physical map of the chromosome of **Neisseria meningitidis** B1940 has been constructed by one- and two-dimensional pulsed-field gel electrophoresis techniques. Complete macrorestriction maps for the enzymes NheI (16 sites), **SgfI** (13 sites), SfiI (11 sites) and I-CeuI (4 sites), as well as a partial restriction map for the restriction enzyme SpeI (15 of c. 28 sites) could be established. Altogether, 59 restriction sites were mapped on a single circular chromosome of 2.3 Mbp. By restriction endonuclease digestion and Southern hybridization of cloned genetic markers, 39 genetic loci were assigned to this map. Comparison with the metabolic maps of **Neisseria** gonorrhoeae MS11-N198 and FA1090 revealed a high degree of conservation in the arrangement of gene loci among these two species, although four out of 24 genetic loci are located at different chromosomal positions, indicating several genomic rearrangements.
Tags: Support, Non-U.S. Gov't
Descriptors: Chromosome Mapping; *Chromosomes, Bacterial--genetics--GE; *Genome, Bacterial; * **Neisseria meningitidis** --genetics--GE; DNA Restriction Enzymes--metabolism--ME; **Neisseria meningitidis** --isolation and purification--IP; Restriction Mapping
Enzyme No.: EC 3.1.21 (DNA Restriction Enzymes)
Record Date Created: 19961205
Record Date Completed: 19961205

8/9/2
DIALOG(R)File 155:MEDLINE(R)

10260590 96062220 PMID: 7592413
The physical map of the chromosome of a serogroup A strain of Neisseria meningitidis **shows complex rearrangements relative to the chromosomes of the two mapped strains of the closely related species N. gonorrhoeae.**
Dempsey J A; Wallace A B; Cannon J G
Department of Microbiology and Immunology, University of North Carolina School of Medicine, Chapel Hill 27599, USA.
Journal of bacteriology (UNITED STATES) Nov 1995, 177 (22) p6390-400, ISSN 0021-9193 Journal Code: 2985120R
Contract/Grant No.: AI23830; AI; NIAID; AI28807; AI; NIAID
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Subfile: INDEX MEDICUS
A physical map of the chromosome of N. **meningitidis** Z2491 (serogroup A, subgroup IV-1) has been constructed. Z2491 DNA was digested with NheI, SpeI, **SgfI** , PacI, BglII, or PmeI, resulting in a limited number of fragments that were resolved by contour-clamped homogeneous electric field (CHEF) electrophoresis. The estimated genome size for this strain was 2,226 kb. To construct the map, probes corresponding to single-copy genes or sequences were used on Southern blots of chromosomal DNA digested with the different mapping enzymes and subjected to CHEF electrophoresis. By determining which fragments from different digests hybridized to each specific probe, it was possible to walk back and forth between digests to form a circular macrorestriction map. The intervals between mapped restriction sites range from 10 to 143 kb in size. A total of 117 markers have been placed on the map; 75 represent identified genes, with the remaining markers defined by anonymous cloned fragments of **neisserial** DNA. Comparison of the arrangement of genetic loci in Z2491 with that in

gonococcal strain FA1090, for which a physical map was previously constructed, revealed complex genomic rearrangements between the two strains. Although gene order is generally conserved over much of the chromosome, a region of approximately 500 kb shows translocation and/or inversion of multiple blocks of markers between the two strains. Even within the relatively conserved portions of the maps, several genetic markers are in different positions in Z2491 and FA1090.

Tags: Support, U.S. Gov't, P.H.S.

Descriptors: Chromosomes, Bacterial; *Gene Rearrangement; * **Neisseria** gonorrhoeae--genetics--GE; * **Neisseria meningitidis** --genetics--GE; *Restriction Mapping; Base Sequence; Chromosome Walking--methods--MT; DNA Probes; Deoxyribonucleases, Type II Site-Specific; Electrophoresis, Gel, Pulsed-Field; Genetic Markers; Inversion (Genetics); Molecular Sequence Data; Translocation (Genetics)

CAS Registry No.: 0 (DNA Probes); 0 (Genetic Markers)

Enzyme No.: EC 3.1.21.4 (Deoxyribonucleases, Type II Site-Specific)

Record Date Created: 19951219

Record Date Completed: 19951219

?logoff hold

```
YSTEM:OS  - DIALOG OneSearch
  File 155:MEDLINE(R)  1966-2003/Oct W4
         (c) format only 2003 The Dialog Corp.
*File 155: Please see HELP NEWS 155 for details about the 2003 reload.
  File 654:US Pat.Full.  1976-2003/Oct 30
         (c) Format only 2003 The Dialog Corp.
*File 654: US published applications now online.  See HELP NEWS 654
for details.  Reassignments current through August 4, 2003.
  File   5:Biosis Previews(R)  1969-2003/Oct W4
         (c) 2003 BIOSIS
*File   5: BIOSIS Previews has been reloaded with major enhancements.
See HELP NEWS005 for more information.
  File  73:EMBASE  1974-2003/Oct W4
         (c) 2003 Elsevier Science B.V.
  File 349:PCT FULLTEXT  1979-2002/UB=20031030,UT=20031023
         (c) 2003 WIPO/Univentio
  File 348:EUROPEAN PATENTS  1978-2003/Oct W04
         (c) 2003 European Patent Office
  File 203:AGRIS  1974-2003/Sep
         Dist by NAL, Intl Copr. All rights reserved
  File  94:JICST-EPlus  1985-2003/Nov W1
         (c)2003 Japan Science and Tech Corp(JST)
  File 444:New England Journal of Med.  1985-2003/Nov W1
         (c) 2003 Mass. Med. Soc.
  File 156:ToxFile  1965-2003/Oct W4
         (c) format only 2003 The Dialog Corporation
*File 156: Please see HELP NEWS 156 for information regarding
the 2003 reload.
  File 357:Derwent Biotech Res.  _1982-2003/Nov W2
         (c) 2003 Thomson Derwent & ISI
*File 357: File is now current.  See HELP NEWS 357.
Alert feature enhanced for multiple files, etc. See HELP ALERT.
  File  35:Dissertation Abs Online  1861-2003/Sep
         (c) 2003 ProQuest Info&Learning
  File 340:CLAIMS(R)/US Patent  1950-03/Oct 30
         (c) 2003 IFI/CLAIMS(R)
*File 340: Enter HELP NEWS340 & HELP ALERTS340 for search,
 display & Alert information.

      Set  Items  Description
      ---  -----  -----------
Cost is in DialUnits
?ds

Set     Items   Description
S1        486   MENINGI? (50N) GONO? (50N) LACTAMIC?
S2        343   RD (unique items)
S3        202   S2 AND (DNA? OR NUCLEIC? OR NUCLEOTID? OR NUCLEIC?)
S4        208   S2 AND (PROBE? OR PRIMER? OR OLIGONUCLEI? OR CDNA? OR POLY-
              NUCLEOT? OR NUCLEOTID? OR NUCLEIC? OR NUCLEAR? OR DNA OR ANTI-
              SENSE?)
S5        111   S4/1996:2003
S6         97   S4 NOT S5
?t s6/9/1-23 54
```

SYSTEM:OS - DIALOG OneSearch
File 155:MEDLINE(R) 1966-2003/Oct W4
(c) format only 2003 The Dialog Corp.
*File 155: Please see HELP NEWS 155 for details about the 2003 reload.
File 654:US Pat.Full. 1976-2003/Oct 30
(c) Format only 2003 The Dialog Corp.
*File 654: US published applications now online. See HELP NEWS 654 for details. Reassignments current through August 4, 2003.
File 5:Biosis Previews(R) 1969-2003/Oct W4
(c) 2003 BIOSIS
*File 5: BIOSIS Previews has been reloaded with major enhancements. See HELP NEWS005 for more information.
File 73:EMBASE 1974-2003/Oct W4
(c) 2003 Elsevier Science B.V.
File 349:PCT FULLTEXT 1979-2002/UB=20031030,UT=20031023
(c) 2003 WIPO/Univentio
File 348:EUROPEAN PATENTS 1978-2003/Oct W04
(c) 2003 European Patent Office
File 203:AGRIS 1974-2003/Sep
Dist by NAL, Intl Copr. All rights reserved
File 94:JICST-EPlus 1985-2003/Nov W1
(c)2003 Japan Science and Tech Corp(JST)
File 444:New England Journal of Med. 1985-2003/Nov W1
(c) 2003 Mass. Med. Soc.
File 156:ToxFile 1965-2003/Oct W4
(c) format only 2003 The Dialog Corporation
*File 156: Please see HELP NEWS 156 for information regarding the 2003 reload.
File 357:Derwent Biotech Res. _1982-2003/Nov W2
(c) 2003 Thomson Derwent & ISI
*File 357: File is now current. See HELP NEWS 357.
Alert feature enhanced for multiple files, etc. See HELP ALERT.
File 35:Dissertation Abs Online 1861-2003/Sep
(c) 2003 ProQuest Info&Learning
File 340:CLAIMS(R)/US Patent 1950-03/Oct 30
(c) 2003 IFI/CLAIMS(R)
*File 340: Enter HELP NEWS340 & HELP ALERTS340 for search, display & Alert information.

Set Items Description
--- ----- -----------
Cost is in DialUnits
?ds

Set Items Description
S1 486 MENINGI? (50N) GONO? (50N) LACTAMIC?
S2 343 RD (unique items)
S3 202 S2 AND (DNA? OR NUCLEIC? OR NUCLEOTID? OR NUCLEIC?)
S4 208 S2 AND (PROBE? OR PRIMER? OR OLIGONUCLEI? OR CDNA? OR POLY-NUCLEOT? OR NUCLEOTID? OR NUCLEIC? OR NUCLEAR? OR DNA OR ANTI-SENSE?)
S5 111 S4/1996:2003
S6 97 S4 NOT S5
?t s6/9/1-23 54

6/9/1 (Item 1 from file: 155)
DIALOG(R)File 155:MEDLINE(R)
(c) format only 2003 The Dialog Corp. All rts. reserv.

08492486 95180702 PMID: 7875573
Identification and characterization of specific sequences encoding pathogenicity associated proteins in the genome of commensal Neisseria species.
Wolff K; Stern A
Department of Biotechnology, TB-Z, Boehringer Mannheim GmbH, Penzberg, Germany.
FEMS microbiology letters (NETHERLANDS) Jan 15 1995, 125 (2-3) p255-63, ISSN 0378-1097 Journal Code: 7705721
Document type: Journal Article

Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Subfile: INDEX MEDICUS

The distribution of distinct sequences in pathogenic and commensal Neisseria species was investigated systematically by dot blot analysis. **Probes** representing the genes of Rmp, pilin and IgA1 protease were found to hybridize exclusively to the chromosomal **DNA** of the pathogenic species, Neisseria **gonorrhoeae** and/or Neisseria **meningitidis** . In contrast, specific sequences for the genes of the porin protein Por and the opacity protein (Opa) were also detected in a panel of commensal Neisseria species such as N. **lactamica** , N. subflava, N. flava, N. mucosa and N. sicca. Using opa-specific oligonucleotides as **probes** in chromosomal blots, the genomes of the commensal Neisseria species show a totally reduced repertoire of cross-hybridizing loci compared to the complex opa gene family of N. **gonorrhoeae** . **DNA** sequence analysis of one opa-related gene derived from N. flava and N. sicca, respectively, revealed a large degree of homology with previously described **gonococcal** and meningococcal genes, e.g., a typical repetitive sequence in the leader peptide and the distribution of the hypervariable and conserved regions. This observation, together with the finding, that the gene is constitutively transcribed, leads to the assumption that some of the commensal Neisseria species may have the potential for the expression of a protein harboring similar functions as the Opa proteins in pathogenic Neisseriae.

Tags: Comparative Study

Descriptors: *Antigens, Bacterial--genetics--GE; *Bacterial Outer Membrane Proteins--genetics--GE; *Genome, Bacterial; *Neisseria--genetics --GE; *Neisseria--pathogenicity--PY; Amino Acid Sequence; Base Sequence; Chromosomes, Bacterial; **DNA Primers** ; **DNA** , Bacterial--genetics--GE; Fimbriae Proteins; Molecular Sequence Data; Neisseria gonorrhoeae--genetics --GE; Neisseria gonorrhoeae--pathogenicity--PY; Neisseria meningitidis --genetics--GE; Neisseria meningitidis--pathogenicity--PY; Oligonucleotide **Probes** ; Sequence Homology, Amino Acid; Serine Endopeptidases--genetics --GE; Species Specificity; Virulence--genetics--GE

Molecular Sequence Databank No.: GENBANK/U12287; GENBANK/U12288

CAS Registry No.: 0 (Antigens, Bacterial); 0 (Bacterial Outer Membrane Proteins); 0 (DNA Primers); 0 (DNA, Bacterial); 0 (Oligonucleotide Probes); 0 (gonococcal protein III); 0 (opacity protein (Neisseria gonorrhoeae)); 147680-16-8 (Fimbriae Proteins)

Enzyme No.: EC 3.4.21 (Serine Endopeptidases); EC 3.4.21.72 (IgA-specific serine endopeptidase)

Record Date Created: 19950404
Record Date Completed: 19950404

6/9/2 (Item 2 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

08371117 95059090 PMID: 7969193

Detection of the tetM determinant in Neisseria gonorrhoeae using a non-radioactively labelled oligonucleotide probe .

Carballo M; Ng L K; Dillon J R

National Laboratory for Sexually Transmitted Diseases, Laboratory Centre for Disease Control, Ottawa, Ontario, Canada.

Molecular and cellular probes (ENGLAND) Jun 1994, 8 (3) p205-8, ISSN 0890-8508 Journal Code: 8709751

Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Subfile: INDEX MEDICUS

Three oligonucleotide **probes** , complementary to tetM sequences, were labelled non-radiometrically using the DIG-oligonucleotide tailing kit and evaluated for their specificity for the detection of plasmid mediated tetracycline resistance in Neisseria **gonorrhoeae** . Only **Probe** 3, 5'-GCT CAA CAA TTC TGT TCC AGC-3', was specific for tetM. It hybridized with the tetM-containing 25.2-MDa plasmids from all of the 232 TRNG and the 130 PP/TRNG isolates used in the study. Its sensitivity, determined by dot-blot

hybridization, was 0.1 pg of pJ13 plasmid **DNA** or 10(4) cells. It did not hybridize with the **DNA** from non-PPNG, CMRNG and tetracycline susceptible isolates from seven other Neisseria species (N. **meningitidis** , N. subflava, N. cinerea, N. **lactamica** , N. sicca, N. mucosa, and N. flavescens), Moraxella spp. and Haemophilus influenzae. **Probe** 3 also hybridized to **DNA** of three tetracycline resistant P. magnus (MIC = 16 micrograms ml-1) isolates which presumptively carried the tetM determinant. Therefore, **probe** 3 can be used by reference laboratories as a confirmatory test for TRNG, as well as isolates from other genera containing the tetM determinant.

Tags: Support, Non-U.S. Gov't

Descriptors: **DNA** , Bacterial--genetics--GE; *Neisseria gonorrhoeae --genetics--GE; *Oligonucleotide **Probes** ; *Polymerase Chain Reaction --methods--MT; Base Sequence; Molecular Sequence Data; Tetracycline Resistance--genetics--GE

CAS Registry No.: 0 (DNA, Bacterial); 0 (Oligonucleotide Probes)

Record Date Created: 19941222

Record Date Completed: 19941222

6/9/3 (Item 3 from file: 155)

DIALOG(R)File 155:MEDLINE(R)

08134698 94200567 PMID: 8150256

Genetic diversity of the iron-binding protein (Fbp) gene of the pathogenic and commensal Neisseria.

Genco C A; Berish S A; Chen C Y; Morse S; Trees D L

Department of Microbiology and Immunology, Morehouse School of Medicine, Atlanta, Georgia 30310.

FEMS microbiology letters (NETHERLANDS) Feb 15 1994, 116 (2) p123-9, ISSN 0378-1097 Journal Code: 7705721

Contract/Grant No.: AI30797; AI; NIAID

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

The pathogenic Neisseria and most commensal Neisseria species produce an iron-binding protein (Fbp) when grown under iron-limited conditions. In the current study, we confirmed the presence of Fbp, as well as **DNA** sequences homologous to the **gonococcal** fbp, in strains of N. **gonorrhoeae** , N. **meningitidis** , N. cinerea, N. **lactamica** , N. subflava, N. kochii and N. polysaccharea. The fbp genes from these strains were amplified by the polymerase chain reaction, digested with StuI or RsaI, and the restriction patterns examined. The patterns for the **gonococcal** and meningococcal fbp were virtually identical; however, variations were observed in the fbp sequences of the commensal Neisseria species. N. flavescens, N. mucosa, N. sicca, N. ovis and Branhamella catarrhalis, did not produce Fbp as detected by sodium dodecyl sulfate-polyacrylamide gel electrophoresis and reactivity with an Fbp specific monoclonal antibody, nor did they hybridize to an fbp-specific **DNA** **probe** .

Tags: Comparative Study; Support, U.S. Gov't, P.H.S.

Descriptors: *Bacterial Proteins--genetics--GE; *Genes, Bacterial --genetics--GE; *Neisseria--genetics--GE; *Variation (Genetics)--genetics --GE; Amino Acid Sequence; Antibodies, Bacterial; Antibodies, Monoclonal; Bacterial Proteins--chemistry--CH; Bacterial Proteins--immunology--IM; Base Sequence; Blotting, Southern; **DNA** **Probes** ; **DNA** , Bacterial --analysis--AN; Molecular Sequence Data; Neisseria gonorrhoeae--genetics --GE; Neisseria meningitidis--genetics--GE; Polymerase Chain Reaction; Restriction Mapping; Sequence Analysis; Species Specificity

CAS Registry No.: 0 (Antibodies, Bacterial); 0 (Antibodies, Monoclonal); 0 (Bacterial Proteins); 0 (DNA Probes); 0 (DNA, Bacterial); 0 (iron-regulated protein, bacterial)

Gene Symbol: fbp

Record Date Created: 19940509

Record Date Completed: 19940509

6/9/4 (Item 4 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

07829627 93285176 PMID: 7685283
Comparison of monoclonal antibody methods and a ribosomal ribonucleic acid probe test for Neisseria gonorrhoeae culture confirmation.
Janda W M; Wilcoski L M; Mandel K L; Ruther P; Stevens J M
Department of Pathology, University of Illinois, Chicago 60612.
European journal of clinical microbiology & infectious diseases - official publication of the European Society of Clinical Microbiology (GERMANY) Mar 1993, 12 (3) p177-84, ISSN 0934-9723 Journal Code: 8804297
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Subfile: INDEX MEDICUS
Recently, a chemiluminescent **nucleic** acid **probe** test that specifically detects the ribosomal ribonucleic acid of Neisseria **gonorrhoeae** has been released for clinical laboratory use (AccuProbe Neisseria **gonorrhoeae**). In this study, three coagglutination tests (**GonoGen** I, Meritec GC, and GC Omni), the **GonoGen** II immunofiltration method and the Micro Trak Neisseria **gonorrhoeae** fluorescent monoclonal antibody test were compared with AccuProbe for identification of **gonococci** . Strains tested (n = 376) included 194 Neisseria **gonorrhoeae** , 82 Neisseria **meningitidis** , 32 Neisseria **lactamica** , 32 Neisseria species, 32 Moraxella catarrhalis, 2 Moraxella spp. and 2 Kingella denitrificans. The **GonoGen** I, Meritec GC and GC Omni coagglutination tests produced clearly positive results for 93.8%, 92.3% and 95.9% of the **gonococci** , respectively. The **GonoGen** II unequivocally identified 91.8% and the MicroTrak fluorescent antibody test identified 90.7% with 2+ or greater fluorescence. AccuProbe identified 100% of the **gonococci** tested. **GonoGen** I and **GonoGen** II were 98% specific, Meritec GC was 99% specific and the specificity of the GC Omni, MicroTrak fluorescent antibody and AccuProbe tests was 100%. While antibody-based tests were reliable when results were clearly interpretable, the AccuProbe was the only confirmatory test that was 100% accurate. Serotyping studies indicate that an array of beta-lactamase positive and negative gonococcal serotypes fail to react with the monoclonal antibody-based tests in general and with the fluorescent antibody test in particular.
Tags: Comparative Study; Human
Descriptors: Antibodies, Monoclonal--immunology--IM; *Neisseria gonorrhoeae--isolation and purification--IP; *RNA **Probes** ; *RNA, Bacterial --genetics--GE; *RNA, Ribosomal--genetics--GE; Fluorescent Antibody Technique; Hemagglutination Tests; Neisseria gonorrhoeae--genetics--GE; Neisseria gonorrhoeae--immunology--IM
CAS Registry No.: 0 (Antibodies, Monoclonal); 0 (RNA Probes); 0 (RNA, Bacterial); 0 (RNA, Ribosomal)
Record Date Created: 19930713
Record Date Completed: 19930713

6/9/5 (Item 5 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

07629605 93084797 PMID: 1452689
Preliminary evaluation of the ligase chain reaction for specific detection of Neisseria gonorrhoeae.
Birkenmeyer L; Armstrong A S
Abbott Laboratories, North Chicago, Illinois 60064.
Journal of clinical microbiology (UNITED STATES) Dec 1992, 30 (12) p3089-94, ISSN 0095-1137 Journal Code: 7505564
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Subfile: INDEX MEDICUS

Rapid identification of Neisseria gonorrhoeae in clinical specimens is essential for effective control. Traditional culture requires a minimum of 24 h, and for some specimens harboring **gonococci** , the **gonococci** fail to grow or are misidentified. The recently described ligase chain reaction (LCR) is a highly specific and sensitive **DNA** amplification technique which was evaluated as an alternative to routine culture. Three LCR **probe** sets were used. Two of the **probe** sets were directed against the multi-copy Opa genes (Omp-II), while the third set was targeted against the multicopy Pilin genes. Each LCR **probe** set was evaluated with 260 microorganisms including 136 global isolates of N. **gonorrhoeae** , 41 isolates of N. **meningitidis** , and 10 isolates of N. **lactamica** ; 26 nonpathogenic Neisseria strains; and 47 isolates of non-Neisseria species that may reside in clinical specimens. Amplification products were detected by using the IMx LCR format (Abbott Laboratories, Abbott Park, Ill.). Strains of N. **gonorrhoeae** were assayed at 270 cells per LCR (approximately 6.7 x 10(4) CFU/ml) with the Opa and Pilin **probes** , producing signals at least 21 and 15 times above background, respectively. In contrast, only background values were observed when testing the **probe** sets with 124 nongonococcal strains at 1.3 x 10(6) cells per LCR (approximately 3.2 x 10(8) CFU/ml). One hundred urogenital specimens were assayed by LCR, and compared with culture, the three **probes** were 100% sensitive (8 of 8) and 97.8% specific (90 of 92), resulting in an agreement of 98% (98 of 100).(ABSTRACT TRUNCATED AT 250 WORDS)

Tags: Human

Descriptors: **DNA** Ligases; *Neisseria gonorrhoeae--genetics--GE; *Neisseria gonorrhoeae--isolation and purification--IP; *Polymerase Chain Reaction--methods--MT; Base Sequence; **DNA Probes** ; **DNA** , Bacterial --genetics--GE; **DNA** , Bacterial--isolation and purification--IP; Evaluation Studies; Gene Amplification; Gonorrhea--diagnosis--DI; Molecular Sequence Data; Polymerase Chain Reaction--statistics and numerical data--SN ; Sensitivity and Specificity

CAS Registry No.: 0 (DNA Probes); 0 (DNA, Bacterial)

Enzyme No.: EC 6.5.1.- (**DNA** Ligases)

Record Date Created: 19930107

Record Date Completed: 19930107

6/9/6 (Item 6 from file: 155)

DIALOG(R)File 155:MEDLINE(R)

07596168 93051225 PMID: 1330818

Sequence analysis and relationships between meningococcal class 3 serotype proteins and other porins from pathogenic and non-pathogenic Neisseria species.

Ward M J; Lambden P R; Heckels J E

Department of Microbiology, Southampton University Medical School, Southampton General Hospital, UK.

FEMS microbiology letters (NETHERLANDS) Jul 15 1992, 73 (3) p283-9, ISSN 0378-1097 Journal Code: 7705721

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

The presence of highly conserved regions within previously determined porin gene sequences from Neisseria **meningitidis** and Neisseria **gonorrhoeae** permitted the construction of oligonucleotide **primers** for PCR amplification of other neisserial porin genes. Although two separate porin genes (porA and porB) are present in N. **meningitidis** only a single fragment, corresponding to porB, could be amplified from this species. The amplified porB genes from four different meningococcal serotypes, which express the class 3 outer membrane protein, were sequenced. Amplified fragments corresponding to porin genes from N. **lactamica** and N. sicca were also sequenced. In common with the known neisserial porins, models of the organisation of the predicted proteins indicated trans-membrane structures with eight surface exposed loops. In the meningococcal class 3 proteins the main regions of sequence variation, which must be responsible for serotype specificity, were located on loops 5 and 7. A phylogenetic

analysis of the family of porins from the Neisseria confirmed the close relationship of the meningococcal class 3 protein with the **gonococcal** PIA protein, while the **gonococcal** PIB protein was shown to be closely related to the N. **lactamica** porin. The close relationship seen between porins of the pathogenic and non-pathogenic Neisseriae identified no obvious virulence-associated regions in the proteins, but did suggest that the current nomenclature for neisserial porin genes may need reviewing.

Tags: Support, Non-U.S. Gov't

Descriptors: *Bacterial Outer Membrane Proteins--metabolism--ME; *Neisseria--genetics--GE; Alleles; Amino Acid Sequence; Base Sequence; Molecular Sequence Data; Neisseria--immunology--IM; Polymerase Chain Reaction; Porins

Molecular Sequence Databank No.: GENBANK/X65461; GENBANK/X65530; GENBANK/X65531; GENBANK/X65532; GENBANK/X65533; GENBANK/X65534

CAS Registry No.: 0 (Bacterial Outer Membrane Proteins); 0 (Porins)

Gene Symbol: por; porA; porB

Record Date Created: 19921218

Record Date Completed: 19921218

6/9/7 (Item 7 from file: 155)

DIALOG(R)File 155:MEDLINE(R)

07560763 93015687 PMID: 1400191

Transformational exchanges in the dihydropteroate synthase gene of Neisseria meningitidis: a novel mechanism for acquisition of sulfonamide resistance.

Radstrom P; Fermer C; Kristiansen B E; Jenkins A; Skold O; Swedberg G

Chemical Center, Lund University, Sweden.

Journal of bacteriology (UNITED STATES) Oct 1992, 174 (20) p6386-93, ISSN 0021-9193 Journal Code: 2985120R

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

The **nucleotide** sequences of the chromosomal dihydropteroate synthase (dhps) genes in sulfonamide-susceptible and sulfonamide-resistant strains of Neisseria meningitidis of serogroups A, B and C were determined. The molecular weights and the amino acid sequences showed similarity to those of all other known dihydropteroate synthase polypeptides. Sequence comparison of the N. meningitidis dhps genes indicated horizontal transfer of **DNA** segments rather than point mutations as the cause for resistance in meningococci. The dhps genes in three of four sulfonamide-resistant meningococci contained identical central regions of 424 bp. Compared with the corresponding genes in susceptible strains, each central region included an insert of 6 bp. In one of the sulfonamide-resistant strains, the dhps gene was similar to the corresponding genes in the sensitive strains in its NH2-terminal and C-terminal parts. Its central region, however, was identical to the corresponding regions of two of the other resistant genes, and thus it could be seen as a hybrid dhps gene. Transformation experiments and mapping of transformed dhps genes indicated the existence of a novel mechanism for the dissemination of sulfonamide resistance in N. **meningitidis** . The origin of the resistance-mediating segment of the gene is unknown, but hybridization results showed the presence of homologous dhps genes in Neisseria **gonorrhoeae** and N. **lactamica** but not in N. subflava or Branhamella catarrhalis.

Tags: Support, Non-U.S. Gov't

Descriptors: *Dihydropteroate Synthase--genetics--GE; *Neisseria meningitidis--drug effects--DE; *Sulfonamides--pharmacology--PD; *Transformation, Bacterial--genetics--GE; Amino Acid Sequence; Base Sequence; Drug Resistance, Microbial--genetics--GE; Genes, Bacterial--genetics--GE; Molecular Sequence Data; Neisseria meningitidis--enzymology--EN; Neisseria meningitidis--genetics--GE; Polymerase Chain Reaction; Restriction Mapping

Molecular Sequence Databank No.: GENBANK/X68062; GENBANK/X68063; GENBANK/X68064; GENBANK/X68065; GENBANK/X68066; GENBANK/X68067; GENBANK/X68068; GENBANK/X68069

CAS Registry No.: 0 (Sulfonamides)

Enzyme No.: EC 2.5.1.15 (Dihydropteroate Synthase)
Gene Symbol: dhps
Record Date Created: 19921113
Record Date Completed: 19921113

6/9/8 (Item 8 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

07344960 92208117 PMID: 1554823
Epidemiology and molecular basis of penicillin-resistant Neisseria meningitidis in Spain: a 5-year history (1985-1989).
Saez-Nieto J A; Lujan R; Berron S; Campos J; Vinas M; Fuste C; Vazquez J A; Zhang Q Y; Bowler L D; Martinez-Suarez J V; et al
Laboratorio de Referencia de Meningococos, Centro Nacional de Microbiologia, Madrid, Spain.
Clinical infectious diseases - an official publication of the Infectious Diseases Society of America (UNITED STATES) Feb 1992, 14 (2) p394-402, ISSN 1058-4838 Journal Code: 9203213
Document type: Journal Article; Review; Review, Tutorial
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Subfile: INDEX MEDICUS
Penicillin-resistant (penr) clinical isolates of Neisseria **meningitidis**, which do not produce beta-lactamase, were first identified in Spain in 1985; the frequency of their recovery, which has been increasing in the past few years, reached 20% in 1989. Serogrouping, determination of serotypes and subtypes, and multilocus enzyme electrophoresis of the penr strains showed an extensive diversity. Resistance is due, at least in part, to a decreased affinity of penicillin-binding protein (PBP) 2 for penicillin. Similar low-affinity forms of PBP 2 are also found in penr isolates of Neisseria **lactamica**, Neisseria polysaccharea, and Neisseria **gonorrhoeae**. Genetic transformation of an N. **meningitidis** type strain to low-level penicillin resistance with **DNA** from resistant meningococci and other Neisseria species resulted in transformants that possessed low-affinity forms of PBP 2. These altered forms of PBP 2 have been shown to arise from recombinational events that replace parts of the PBP 2 gene with the corresponding regions from the PBP 2 genes of commensal Neisseria species. (34 Refs.)
Tags: Human; Support, Non-U.S. Gov't
Descriptors: *Meningitis, Meningococcal--epidemiology--EP; *Meningococcal Infections--epidemiology--EP; *Neisseria meningitidis--drug effects--DE; *Penicillin Resistance--genetics--GE; Hexosyltransferases--genetics--GE; Hexosyltransferases--metabolism--ME; Meningitis, Meningococcal--microbiology--MI; Meningococcal Infections--microbiology--MI; Multienzyme Complexes--genetics--GE; Multienzyme Complexes--metabolism--ME; Neisseria meningitidis--classification--CL; Neisseria meningitidis--genetics--GE; Peptidyltransferase--genetics--GE; Peptidyltransferase--metabolism--ME; Spain--epidemiology--EP; beta-Lactamases--biosynthesis--BI; beta-Lactamases--genetics--GE
CAS Registry No.: 0 (Multienzyme Complexes); 9042-06-2 (peptidoglycan synthetase)
Enzyme No.: EC 2.3.2.12 (Peptidyltransferase); EC 2.4.1.- (Hexosyltransferases); EC 3.5.2.6 (beta-Lactamases)
Gene Symbol: penA
Record Date Created: 19920507
Record Date Completed: 19920507

6/9/9 (Item 9 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

07299344 92162276 PMID: 1536720
Regulation of aspartate carbamoyltransferase in Neisseria and Branhamella species.
Jyssum S

Kaptein W. Wilhelmsen og Frues Bakteriologiske Institutt, University of Oslo, Rikshospitalet, Norway.
APMIS - acta pathologica, microbiologica, et immunologica Scandinavica (DENMARK) Jan 1992, 100 (1) p48-56, ISSN 0903-4641 Journal Code: 8803400
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Subfile: INDEX MEDICUS
The regulatory characteristics of aspartate carbamoyltransferase (ACTase EC 2.1.3.2) from various species of Neisseria and Branhamella have been compared. Great differences in the regulatory nature of the enzymes were observed. ATP and GTP were positive effectors in Neisseria **meningitidis** , N. **gonorrhoeae** and nine other coccal "true neisseriae" species. In four "false neisseriae" species, including Branhamella catarrhalis, no stimulating effect of ATP or GTP was observed. The rod-shaped N. elongata behaved as the "false neisseriae" in these respects, despite its taxonomic affinity to the coccal "true neisseriae" species. Except in N. **meningitidis** and N. **lactamica** , CTP had no distinct stimulatory effect. CTP had a strong inhibitory effect on ACTases from N. elongata and the "false neisseriae" species N. caviae and B. catarrhalis. The inhibitory effect of CTP was weak in N. cinerea, N. denitrificans, and the "false neisseriae" species N. ovis and N. cuniculi. Thus, there was no sharp reflection of taxonomy in the regulation of ACTase by CTP in these groups of bacteria. The apparent [S]0.5 values for aspartate and carbamoyl phosphate, displayed for five of the eighteen species, showed great variability with [S]0.5 values for aspartate ranging from 6 to 34, and for carbamoyl phosphate from 2 to 9. Treatment of the enzyme from the main test microbe N. meningitidis strain M1 by heat or para-chloromercuribenzoate (pCMB) showed that both the catalytic and the regulatory functions decreased in parallel as in the class A enzymes found in species of Pseudomonas. An estimation of the molecular weight (Mr) of the ACTase enzyme from N. meningitidis showed it to be about 295,000, which resembles the class B enzymes found in the Enterobacteriaceae.
Tags: Comparative Study
Descriptors: *Aspartate Carbamoyltransferase--metabolism--ME; *Moraxella --enzymology--EN; *Neisseria--enzymology--EN; Aspartate Carbamoyltransferase--chemistry--CH; Aspartic Acid--metabolism--ME; Carbamyl Phosphate --metabolism--ME; Chloromercuribenzoates--chemistry--CH; Enzyme Activation; Heat; Molecular Weight; **Nucleotides** --pharmacology--PD; p-Chloromercuribenzoic Acid
CAS Registry No.: 0 (Chloromercuribenzoates); 0 (Nucleotides); 56-84-8 (Aspartic Acid); 59-85-8 (p-Chloromercuribenzoic Acid); 590-55-6 (Carbamyl Phosphate)
Enzyme No.: EC 2.1.3.2 (Aspartate Carbamoyltransferase)
Record Date Created: 19920331
Record Date Completed: 19920331

6/9/10 (Item 10 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

06917986 91158313 PMID: 2127349
Neisseria lactamica and Neisseria polysaccharea as possible sources of meningococcal beta-lactam resistance by genetic transformation.
Saez-Nieto J A; Lujan R; Martinez-Suarez J V; Berron S; Vazquez J A; Vinas M; Campos J
Laboratorio de Referencia de Meningococos, Centro Nacional de Microbiologia, Madrid, Spain.
Antimicrobial agents and chemotherapy (UNITED STATES) Nov 1990, 34 (11) p2269-72, ISSN 0066-4804 Journal Code: 0315061
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Subfile: INDEX MEDICUS
We studied the susceptibilities of relatively penicillin G-resistant and

-susceptible strains of Neisseria **meningitidis** , as well as Neisseria **lactamica** and Neisseria polysaccharea, to penicillin, ampicillin, and several cephalosporins. The MICs of penicillin, ampicillin, cephalothin, and cefuroxime for moderately resistant meningococci have increased two- to sixfold in relation to MICs for susceptible strains. For these strains of meningococci, N. **lactamica** , and N. polysaccharea, penicillin, ampicillin, cephalothin, and cefuroxime MICs for 50 and 90% of strains were similar. By genetic transformation of a penicillin-susceptible strain of N. **meningitidis** to low-level penicillin resistance with **DNA** from penicillin-resistant strains of N. **meningitidis** , N. **lactamica** , N. polysaccharea, and N. **gonorrhoeae** , isogenic strains with the same pattern of resistance to beta-lactams were obtained, suggesting that these commensal Neisseria spp. could be the source of meningococcal resistance genes.

Tags: Support, Non-U.S. Gov't

Descriptors: *Antibiotics, Lactam--pharmacology--PD; *Drug Resistance, Microbial--genetics--GE; *Neisseria--genetics--GE; *Neisseria meningitidis --genetics--GE; **DNA** , Bacterial--genetics--GE; **DNA** , Bacterial --isolation and purification--IP; Penicillin Resistance--genetics--GE; Phenotype; Transformation, Genetic

CAS Registry No.: 0 (Antibiotics, Lactam); 0 (DNA, Bacterial)

Record Date Created: 19910408

Record Date Completed: 19910408

6/9/11 (Item 11 from file: 155)

DIALOG(R)File 155:MEDLINE(R)

06714030 90340048 PMID: 2116567

Distribution of gonococcal lipopolysaccharide biosynthesis genes among strains of Neisseria gonorrhoeae and other neisserial species.

Palermo-Dilts D A; Silver L E; Clark V L

Department of Microbiology and Immunology, School of Medicine and Dentistry, University of Rochester, NY 14642.

Microbial pathogenesis (ENGLAND) Mar 1990, 8 (3) p227-33, ISSN 0882-4010 Journal Code: 8606191

Contract/Grant No.: R01 AI 11709; AI; NIAID

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

A plasmid, pTME6, containing Neisseria **gonorrhoeae** lipopolysaccharide biosynthesis genes was used as a **probe** to analyze **DNA** from strains of N. **gonorrhoeae** , N. **meningitidis** and various commensal Neisseria by Southern blotting. Chromosomal **DNA** from 26 **gonococcal** strains **probed** with 32P-labeled pTME6 produced five different hybridization patterns. No correlation between hybridization pattern and auxotype, serotype, serum sensitivity or SDS-urea-PAGE migration of LPS was observed. **DNA** from strains of N. **meningitidis** , N. **lactamica** and N. cinerea, but not other commensal Neisseria species, hybridized strongly to pTME6.

Tags: Support, U.S. Gov't, P.H.S.

Descriptors: **DNA** , Bacterial--genetics--GE; *Genes, Bacterial; *Lipopolysaccharides--genetics--GE; *Neisseria--genetics--GE; *Neisseria gonorrhoeae--genetics--GE; *Streptococcus--genetics--GE; Lipopolysaccharides--biosynthesis--BI; Neisseria gonorrhoeae--growth and development--GD; **Nucleic** Acid Hybridization; Restriction Mapping; Streptococcus--growth and development--GD

CAS Registry No.: 0 (DNA, Bacterial); 0 (Lipopolysaccharides)

Record Date Created: 19900912

Record Date Completed: 19900912

6/9/12 (Item 12 from file: 155)

DIALOG(R)File 155:MEDLINE(R)

06560016 90185237 PMID: 2155857

DNA **methylation in Neisseria gonorrhoeae and other Neisseriae.**
Ritchot N; Roy P H
Departement de Biochimie, Faculte des Sciences et de Genie, Universite Laval, Sainte-Foy, Canada.
Gene (NETHERLANDS) Jan 31 1990, 86 (1) p103-6, ISSN 0378-1119 Journal Code: 7706761
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Subfile: INDEX MEDICUS

It has been reported in the literature that Neisseria gonorrhoeae **DNA** is modified by the methyltransferases (MTases) M.NgoI, M.NgoII, and M.NgoIII, as well as three other cytosine MTases and one adenine MTase, even if the corresponding restriction endonucleases are not present. We envisioned the possibility of cloning one of the N. gonorrhoeae MTase-encoding genes for use as a species-specific **DNA probe** . We therefore undertook a survey of methylation patterns of several clinical isolates of N. gonorrhoeae and N. **meningitidis** as well as ATCC strains of other Neisseriae. We found, from digestion patterns with isoschizomers, one N. **gonorrhoeae** strain that lacked M.NgoII and two that lacked M.NgoIII. All N. **meningitidis** strains (save one) were resistant to digestion with NlaIV thus possessing an MTase like NgoV, and one was resistant to SstII, thus having an NgoIII-like MTase. None were resistant to isoschizomers of NgoI, NgoIII and NgoIV. Some other Neisseriae had an MTase with NlaIV (NgoV) specificity, but none had NgoI, II, III or IV specificity, except for the Branhamella-like N. caviae-ovis group and N. **lactamica** where these specificities were present in at least one strain of this group. Therefore, among the Neisseriae other than N. caviae only M.NgoI is N. **gonorrhoeae** -specific.

Descriptors: **DNA** Modification Methylases--metabolism--ME; *Neisseria --genetics--GE; *Neisseria gonorrhoeae--genetics--GE; **DNA** Restriction Enzymes--metabolism--ME; **DNA** , Bacterial--metabolism--ME; Methylation; Neisseria--enzymology--EN; Neisseria gonorrhoeae--enzymology--EN
CAS Registry No.: 0 (DNA, Bacterial)
Enzyme No.: EC 2.1.1.- (**DNA** Modification Methylases); EC 3.1.21 (**DNA** Restriction Enzymes)
Record Date Created: 19900426
Record Date Completed: 19900426

6/9/13 (Item 13 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

05906542 88260884 PMID: 2455211
Common mechanism controlling phase and antigenic variation in pathogenic neisseriae.
Stern A; Meyer T F
Max-Planck-Institut fur Biologie, Infektgenetik, Tubingen, FRG.
Molecular microbiology (ENGLAND) Jul 1987, 1 (1) p5-12, ISSN 0950-382X Journal Code: 8712028
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Subfile: INDEX MEDICUS

The expression of the Neisseria **gonorrhoeae** opacity protein (Op, protein II), a major antigenic determinant of the outer membrane, is subject to frequent phase transitions. At least nine expression loci (opaE) are involved in the production of a large number of serologically distinct Op types. Using opa-specific oligonucleotides as **probes** in genomic blots, we detect Op-related gene sequences (opr) in N. **meningitidis** as well as in N. **lactamica** . **DNA** sequence analysis of such opr genes derived from N. **meningitidis** reveals distinct regions of homology with **gonococcal** opa E genes. As shown in the immunoblot, the proteins encoded by opa and opr are serologically related. Like the opaE genes, the 5'-coding sequences of the opr genes include a repetitive sequence composed of pentameric CTCTT units. The number of these coding repeat (CR) units is variable. This

finding, together with the observation that all opr genes are constitutively transcribed, regardless of the status of protein production, suggests a translational control mechanism identical to that of the opa genes in **gonococci** . The related structures and control mechanisms of opa and opr genes imply a general significance of their gene products for the pathogenic character of the investigated Neisseria species.

Tags: Support, Non-U.S. Gov't

Descriptors: *Antigens, Bacterial--genetics--GE; *Bacterial Outer Membrane Proteins--genetics--GE; *Genes, Bacterial; *Genes, Structural; *Neisseria--genetics--GE; Amino Acid Sequence; Antigens, Bacterial --immunology--IM; Base Sequence; Epitopes--genetics--GE; Molecular Sequence Data; Neisseria gonorrhoeae--genetics--GE; Neisseria meningitidis--genetics --GE; Species Specificity

Molecular Sequence Databank No.: GENBANK/X06445; GENBANK/X06446

CAS Registry No.: 0 (Antigens, Bacterial); 0 (Bacterial Outer Membrane Proteins); 0 (Epitopes); 0 (opacity protein (Neisseria gonorrhoeae))

Record Date Created: 19880811

Record Date Completed: 19880811

6/9/14 (Item 14 from file: 155)

DIALOG(R)File 155:MEDLINE(R)

05724081 88077454 PMID: 3120761

Deoxyribonucleic acid relatedness among Neisseria gonorrhoeae , **N.** meningitidis , **N.** lactamica , **N. cinerea and "Neisseria polysaccharea".**

Guibourdenche M; Popoff M Y; Riou J Y

Laboratoire des Neisseria, Institut Pasteur, Paris.

Annales de l'Institut Pasteur. Microbiology (FRANCE) Sep-Oct 1986, 137B (2) p177-85, ISSN 0769-2609 Journal Code: 8701984

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

Deoxyribonucleic acid relatedness studies (S1 nuclease method with DE-81 filters method) indicated that Neisseria **gonorrhoeae** , N. **meningitidis** , N. **lactamica** and "N. polysaccharea" form a single genospecies, in which four subspecies can be delineated. However, from a clinical and practical viewpoint, it seems desirable to maintain N. **gonorrhoeae** , N. **meningitidis** , N. **lactamica** and "N. polysaccharea" as separate species. N. cinerea is a valid species, closely related to N. **gonorrhoeae** , N. **meningitidis** , N. **lactamica** and "N. polysaccharea". These five species were 0 to 46% related to the other known species of the genus Neisseria.

Tags: Comparative Study

Descriptors: **DNA** , Bacterial; *Neisseria--classification--CL; Neisseria --genetics--GE; Neisseria gonorrhoeae--classification--CL; Neisseria gonorrhoeae--genetics--GE; Neisseria meningitidis--classification--CL; Neisseria meningitidis--genetics--GE; **Nucleic** Acid Hybridization

CAS Registry No.: 0 (DNA, Bacterial)

Record Date Created: 19880126

Record Date Completed: 19880126

6/9/15 (Item 15 from file: 155)

DIALOG(R)File 155:MEDLINE(R)

05485698 87164490 PMID: 2881892

Distribution of specific DNA **sequences among pathogenic and commensal Neisseria species.**

Aho E L; Murphy G L; Cannon J G

Infection and immunity (UNITED STATES) Apr 1987, 55 (4) p1009-13, ISSN 0019-9567 Journal Code: 0246127

Contract/Grant No.: AI15036; AI; NIAID

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed
Subfile: INDEX MEDICUS

Several traits, including pili and the outer membrane proteins P.II and H.8, have been associated with pathogenic Neisseria species. We examined several Neisseria species for **DNA** sequence homology to cloned pilin, P.II, and H.8 genes. Strains of Neisseria **gonorrhoeae** and N. **meningitidis** showed hybridization to all of these genes. Commensal strains showed little hybridization to any of these genes. Strains of N. **lactamica** and N. cinerea showed intermediate patterns of hybridization. Generally, organisms that expressed a given trait showed **DNA** homology to the corresponding cloned gene. However, we observed pili on some commensal strains that did not show hybridization to the cloned **gonococcal** pilin gene.

Tags: Support, U.S. Gov't, Non-P.H.S.; Support, U.S. Gov't, P.H.S.

Descriptors: *Bacterial Outer Membrane Proteins--genetics--GE; *Neisseria --genetics--GE; Fimbriae Proteins; Fimbriae, Bacterial; Genes, Structural; Neisseria--pathogenicity--PY; Neisseria gonorrhoeae--genetics--GE; Neisseria meningitidis--genetics--GE; **Nucleic** Acid Hybridization; Sequence Homology, **Nucleic** Acid

CAS Registry No.: 0 (Bacterial Outer Membrane Proteins); 147680-16-8 (Fimbriae Proteins)

Record Date Created: 19870430
Record Date Completed: 19870430

6/9/16 (Item 16 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

05379832 87058180 PMID: 3097079

Homology of cryptic plasmid of Neisseria gonorrhoeae **with plasmids from Neisseria** meningitidis **and Neisseria** lactamica.

Ison C A; Bellinger C M; Walker J

Journal of clinical pathology (ENGLAND) Oct 1986, 39 (10) p1119-23, ISSN 0021-9746 Journal Code: 0376601

Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Subfile: AIM; INDEX MEDICUS

DNA **probe** hybridisation was used to examine the relation between the cryptic plasmid from Neisseria **gonorrhoeae** and plasmids carried by pharyngeal isolates of Neisseria **meningitidis** and Neisseria **lactamica**. The complete **gonococcal** cryptic plasmid and HinfI derived digestion fragments subcloned into Escherichia coli were used to **probe** Southern blots of plasmid extracts. Homology was found to a plasmid of approximate molecular weight 4.5 kilobase pairs (Kb) but not to plasmids of less than 3.2 Kb or 6.5 Kb. Eleven of 16 strains of N **meningitidis** and two of six strains of N **lactamica** carried plasmids that showed strong hybridisation with the 4.2 Kb **gonococcal** plasmid. Hybridisation of plasmids from non-**gonococcal** species of neisseria with the **gonococcal** cryptic plasmid indicates that caution should be taken when using the cryptic plasmid as a diagnostic **probe** for **gonorrhoea**.

Descriptors: *Neisseria--genetics--GE; *Plasmids; **DNA**, Bacterial; Electrophoresis, Agar Gel; Molecular Weight; Neisseria--classification--CL; Neisseria gonorrhoeae--genetics--GE; Neisseria meningitidis--genetics--GE; **Nucleic** Acid Hybridization

CAS Registry No.: 0 (DNA, Bacterial); 0 (Plasmids)

Record Date Created: 19870105
Record Date Completed: 19870105

6/9/17 (Item 17 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

05101464 86101901 PMID: 3936398

[Enzymatic profile and plasmid content of Neisseria polysaccharеae]

Profil enzymatique et contenu plasmidique de "Neisseria polysaccharеae".

Delmas C; Prere M F; Fayet O; Lareng M B; Dabernat H
Annales de l'Institut Pasteur. Microbiologie (FRANCE) Jul-Aug 1985, 136B (1) p29-38, ISSN 0769-2609 Journal Code: 8503044
Document type: Journal Article ; English Abstract
Languages: FRENCH
Main Citation Owner: NLM
Record type: Completed
Subfile: INDEX MEDICUS

The enzymatic profile of "Neisseria polysaccharеae" was determined by using chromogenic substrate (API System), and was compared to that of N. **meningitidis** , N. **gonorrhoeae** and N. **lactamica** . The tested classes of enzymes were aminopeptidase, proteases, esterases, lipases, glycosidases, phosphatase and phosphoamidase. "N. polysaccharеae" exhibited various aminopeptidase and protease activities and a strong esterase activity. No lipase and glycosidase activities were detected by the tested substrates. The strains of "N. polysaccharеae" differed from that of N. **meningitidis** in the presence of hydroxyproline aminopeptidase and the lack of gamma-glutamyl-transferase activity. Five strains harboured extrachromosomal elements. The plasmids were of 4.2 Kb in size in four cases and of more than 40 Kb in four cases. Three strains simultaneously harboured these two plasmids. This plasmid content is another characteristic of strains of this new taxon. No phenotypic modification was observed in plasmid-containing strains.

Descriptors: *Neisseria--enzymology--EN; *Plasmids; **DNA** --analysis--AN; Electrophoresis, Agar Gel; Neisseria--classification--CL; Neisseria --genetics--GE; Neisseria gonorrhoeae--enzymology--EN; Neisseria meningitidis--enzymology--EN
CAS Registry No.: 0 (Plasmids); 9007-49-2 (DNA)
Record Date Created: 19860130
Record Date Completed: 19860130

6/9/18 (Item 18 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

05084041 86084472 PMID: 3941006
Distribution of an antigenically related iron-regulated protein among the Neisseria spp.
Mietzner T A; Barnes R C; JeanLouis Y A; Shafer W M; Morse S A
Infection and immunity (UNITED STATES) Jan 1986, 51 (1) p60-8, ISSN 0019-9567 Journal Code: 0246127
Contract/Grant No.: AI 13571; AI; NIAID; AI 22148; AI; NIAID
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Subfile: INDEX MEDICUS

Several iron-regulated proteins of Neisseria gonorrhoeae have been reported. One of these, a 37,000-molecular-weight protein (37K protein), appears to be common to all gonococcal isolates. Recently, the occurrence of a similar protein has also been noted in N. **meningitidis** . The gonococcal 37K protein has been purified and used to produce both rabbit monospecific antiserum and murine monoclonal antibodies. Using these antibody reagents, we analyzed 57 strains from nine species of Neisseria and the closely related organism Branhamella catarrhalis for the presence of proteins antigenically related to the **gonococcal** 37K protein. Strains grown on medium with low iron content were **probed** for antigenic reactivity by Western blot techniques and an enzyme-linked immunosorbent assay. Proteins which cross-reacted with the rabbit monospecific antiserum were designated as AgR-37K proteins. The data indicated that the AgR-37K proteins were conserved among the 40 strains of N. **gonorrhoeae** , N. **meningitidis** , N. **lactamica** , and N. cinerea tested. Seventeen strains from other species of Neisseria and Branhamella did not express AgR-37K proteins with the exception of one N. subflava isolate. All AgR-37K proteins appeared to be regulated by the amount of available iron in the growth medium. Murine monoclonal antibodies were used to **probe** the antigenic heterogeneity of the AgR-37K proteins from different Neisseria spp. Two of seven monoclonal antibodies were broadly cross-reactive,

recognizing the AgR-37K proteins from all species examined. The remaining five monoclonal antibodies were more discriminating, recognizing the AgR-37K proteins from certain species. The antigenic conservation of these AgR-37K proteins, particularly among the pathogenic members of the genus Neisseria, may imply that these proteins serve a common function in pathogenicity.

Tags: Support, U.S. Gov't, P.H.S.

Descriptors: *Bacterial Proteins--metabolism--ME; *Membrane Proteins --metabolism--ME; *Neisseria--genetics--GE; Antibodies, Bacterial --immunology--IM; Antibodies, Monoclonal--immunology--IM; Antibody Specificity; Antigens, Bacterial--immunology--IM; Bacterial Proteins --genetics--GE; Bacterial Proteins--immunology--IM; Cross Reactions; Gene Expression Regulation; Iron--physiology--PH; Membrane Proteins--genetics --GE; Membrane Proteins--immunology--IM; Molecular Weight; Neisseria --immunology--IM; Species Specificity

CAS Registry No.: 0 (Antibodies, Bacterial); 0 (Antibodies, Monoclonal); 0 (Antigens, Bacterial); 0 (Bacterial Proteins); 0 (Membrane Proteins); 7439-89-6 (Iron)

Record Date Created: 19860219

Record Date Completed: 19860219

6/9/19 (Item 19 from file: 155)

DIALOG(R)File 155:MEDLINE(R)

04008551 83137285 PMID: 6219168

Differentiation of neisseriaceae by isoenzyme electrophoresis.

Braude A I; McCutchan J A; Ison C; Sargeaunt P R

Journal of infectious diseases (UNITED STATES) Feb 1983, 147 (2) p247-51, ISSN 0022-1899 Journal Code: 0413675

Contract/Grant No.: AI11643; AI; NIAID

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: AIM; INDEX MEDICUS

Analysis of 71 strains of Neisseriaceae by starch-gel electrophoresis of hexokinase, phosphoglucomutase, glucose phosphate isomerase, and L-malate-nicotinamide adenine dinucleotide phosphate oxidoreductase showed that all **gonococci** and all memingococci have a characteristic hexokinase isoenzyme that is specific for each species and clearly distinguishes meningococci and **gonococci** from each other and from other species of Neisseriaceae. Strains of **gonococci** that were transformed into maltose utilizers by **DNA** from Neisseria **lactamica** and Neisseria **meningitidis** showed no change in the isoenzymes so that they could still be differentiated from meningococci and other Neisseriaceae by isoenzyme electrophoresis. In view of the limited sensitivity and specificity of conventional tests for the identification of **gonococci** and the possibility that **gonococci** may be transformed into maltose utilizers by **DNA** from normal throat flora, electrophoresis of hexokinase isoenzymes should be useful for the precise laboratory identification of the pathogenic neisseriae, especially those from atypical sites and those giving indeterminate reactions.

Tags: Support, Non-U.S. Gov't; Support, U.S. Gov't, P.H.S.

Descriptors: *Isoenzymes--metabolism--ME; *Neisseria--classification--CL ; Electrophoresis, Starch Gel; Glucose-6-Phosphate Isomerase--metabolism --ME; Hexokinase--metabolism--ME; Malate Dehydrogenase--metabolism--ME; Maltose--metabolism--ME; Neisseria--enzymology--EN; Neisseria--metabolism --ME; Phosphoglucomutase--metabolism--ME; Transformation, Bacterial

CAS Registry No.: 0 (Isoenzymes); 69-79-4 (Maltose)

Enzyme No.: EC 1.1.1.37 (Malate Dehydrogenase); EC 2.7.1.1 (Hexokinase); EC 5.3.1.9 (Glucose-6-Phosphate Isomerase); EC 5.4.2.2 (Phosphoglucomutase)

Record Date Created: 19830407

Record Date Completed: 19830407

6/9/20 (Item 20 from file: 155)

DIALOG(R)File 155:MEDLINE(R)

03903173 83031326 PMID: 6813359
Acquisition of new genes by oral Neisseria.
Ison C; Glynn A A; Bascomb S
Journal of clinical pathology (ENGLAND) Oct 1982, 35 (10) p1153-7, ISSN 0021-9746 Journal Code: 0376601
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Subfile: AIM; INDEX MEDICUS

It is suggested that part of the increased pharyngeal carriage of meningococci reported in patients with **gonorrhoea** is due to misidentification of **gonococci** which have been transformed to maltose fermenters by **DNA** from normal throat flora. The distribution of specific aminopeptidases in strains of **gonococci** , meningococci isolated from the throat and meningococci from systemic infections is consistent with this view. **Gonococci** oxidising maltose and **gonococci** with gamma-L-glutamyl aminopeptidase activity, both factors regarded as typical of Neisseria **meningitidis** , can be produced in vitro by transformation with **DNA** from N **lactamica** and N **meningitidis** . The clinical and theoretical implications of such changes are discussed.

Tags: Human; Male; Support, Non-U.S. Gov't
Descriptors: *Genes, Bacterial; *Neisseria gonorrhoeae--genetics--GE; *Neisseria meningitidis--genetics--GE; *Pharynx--microbiology--MI; Aminopeptidases--metabolism--ME; Asparaginase--metabolism--ME; Glutaminase --metabolism--ME; Microbial Sensitivity Tests; Neisseria gonorrhoeae--drug effects--DE; Neisseria meningitidis--drug effects--DE; Oleic Acids --pharmacology--PD; Phenotype; Transformation, Bacterial
CAS Registry No.: 0 (Oleic Acids)
Enzyme No.: EC 3.4.11 (Aminopeptidases); EC 3.5.1.1 (Asparaginase); EC 3.5.1.2 (Glutaminase)
Record Date Created: 19821221
Record Date Completed: 19821221

6/9/21 (Item 21 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

03827668 82239743 PMID: 6808013
Laboratory diagnosis of gonococcal infection by genetic transformation.
Butler L O; Knight R D
Journal of clinical microbiology (UNITED STATES) May 1982, 15 (5) p810-4, ISSN 0095-1137 Journal Code: 7505564
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Subfile: INDEX MEDICUS

The transformation test for the detection of infection by Neisseria **gonorrhoeae** has been examined using pro **gonococci** as recipients and **DNA** preparations from 912 clinical isolates and from 240 direct swab specimens as donors. The reliability of the method was checked with **DNA** from clinical isolates; 82% of the N. **meningitidis** from throat swab specimens were capable of transforming the **gonococcal** recipients, but after identification of the meningococcus by the aminopeptidase profile, the transformation test was then 99.5% positive for the **gonococcus** with virtually no false-positives. The only other organism to give a positive reaction was N. **lactamica** , which occurred once in 912 specimens. When applied directly to swab specimens, the reliability of the test was reduced, but this may have been related to variability of the specimen itself. However, 7 of 15 specimens which were microscopically suspected to be **gonococci** but unculturable were positive; also, 9 out of 38 unculturable specimens that were not even suspected to be **gonococci** were positive. Hence the test was able to identify the presence of **gonococci** that were unculturable. The aminopeptidase activities were not sensitive

enough to be detected in the direct swab specimens, and neither cys nor leu auxotrophs were suitable as recipients to give a differentiation between N. gonorrhoeae and N. **meningitidis** . Evidence was obtained which would support the proposition that the transfer of genetic material between N. gonorrhoeae and N. **meningitidis** may occur.
Tags: Human; Support, Non-U.S. Gov't
Descriptors: *Bacteriological Techniques; *Gonorrhea--diagnosis--DI; *Transformation, Bacterial; Aminopeptidases--metabolism--ME; Neisseria gonorrhoeae--enzymology--EN; Neisseria gonorrhoeae--genetics--GE; Neisseria meningitidis--genetics--GE
Enzyme No.: EC 3.4.11 (Aminopeptidases)
Record Date Created: 19820910
Record Date Completed: 19820910

6/9/22 (Item 22 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

02179265 76133398 PMID: 814781
Radiorespirometric studies in genus Neisseria. 2. The catabolism of glutamate and fumarate.
Holten E
Acta pathologica et microbiologica Scandinavica. Section B, Microbiology (DENMARK) Feb 1976, 84 (1) p1-8, ISSN 0105-0656 Journal Code: 7508472
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Subfile: INDEX MEDICUS
The catabolism of glutamate and fumarate was studied by radiorespirometry in selected Neisseria species. The tricarboxylic acid cycle is functioning in all species tested, in spite of the known absence of in vitro malate dehydrogenase activity in N. **meningitidis** , N. **gonorrhoeae** and N. cinerea. The results imply a pyridine **nucleotide** independent oxidation of malate. The oxidation of glutamate is less complete in the presence of phosphate. In N. **meningitidis** , N. perflava, N. flava, N. subflava and N. **lactamica** the catabolism of fumarate was slow and incomplete in the absence of glutamate.
Descriptors: *Fumarates--metabolism--ME; *Glutamates--metabolism--ME; *Neisseria--metabolism--ME; Carbon Dioxide--metabolism--ME; Citric Acid Cycle; Malate Dehydrogenase--metabolism--ME; Neisseria--enzymology--EN; Neisseria gonorrhoeae--metabolism--ME; Neisseria meningitidis--metabolism --ME
CAS Registry No.: 0 (Fumarates); 0 (Glutamates); 124-38-9 (Carbon Dioxide)
Enzyme No.: EC 1.1.1.37 (Malate Dehydrogenase)
Record Date Created: 19760409
Record Date Completed: 19760409

6/9/23 (Item 23 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

02117664 76069099 PMID: 811645
Intrageneric transformation of neisseria gonorrhoeae and neisseria perflava to streptomycin resistance and nutritional independence.
Siddiqui A; Goldberg I D
Journal of bacteriology (UNITED STATES) Dec 1975, 124 (3) p1359-65, ISSN 0021-9193 Journal Code: 2985120R
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Subfile: INDEX MEDICUS
Auxotrophic mutants of Neisseria gonorrhoeae and Neisseria perflava were transformed to prototrophy using homologous and heterologous

deoxyribonucleic acid (**DNA**). Within either species the efficiencies of transformation for nutritional markers were found to be very similar to the values obtained for transformation to streptomycin resistance. The number of transformants in the interspecific N. perflava (donor) - - leads to N. gonorrhoeae (recipient) cross was 100-fold lower than the number obtained in the intraspecific N. gonorrhoeae - - leads to N. gonorrhoeae cross for streptomycin resistance, as well as for several nutritional markers. In the reciprocal experiment the difference in the number of transformants in the interspecific N. **gonorrhoeae** - - leads to N. perflava cross and the number obtained in the intraspecific N. perflava - - leads to N. perflava cross varied from 600 to 1,000-fold for the streptomycin resistance marker. Of greater interest was the finding that N. perflava auxotrophs, although transformable to prototrophy with wild-type N. perflava **DNA** , were not transformed to nutritional independence by gnoncoccal **DNA** . These same mutants were transformable to streptomycin resistance using the heterologous **gonococcal** **DNA** . When the DNAs of N. **meningitidis** , N. flava, and N. **lactamicus** were used to transform N. **gonorrhoeae** to prototrophy or streptomycin resistance, the transformation frequencies obtained fell along a gradient that in general reflected taxonomic relationships. On the other hand, with N. perflava as the recipient for these same DNAs, only N. flava **DNA** could transform auxotrophs to prototrophy, although transformation to streptomycin resistance occurred in all cases. **DNA** from N. perflava - - leads to N. **gonorrheae** streptomycin-resistant or Ade+ intergenotic transformants transformed N. **gonorrhoeae** cells at a 100-fold-higher efficiency than did **DNA** from N. perflava. Our findings suggest that (i) N. **gonorrhoeae** and N. perflava are more closely related than hitherto suspected and (ii) N. perflava is more selective with respect to heterologous **DNA** than is N. gonorrhoeae.

Tags: Support, U.S. Gov't, P.H.S.

Descriptors: *Neisseria; *Neisseria gonorrhoeae; *Transformation, Genetic ; Amino Acids--metabolism--ME; **DNA** , Bacterial; Drug Resistance, Microbial ; Mutation; Neisseria--drug effects--DE; Neisseria--metabolism--ME; Neisseria gonorrhoeae--drug effects--DE; Neisseria gonorrhoeae--metabolism --ME; Species Specificity; Streptomycin--pharmacology--PD

CAS Registry No.: 0 (Amino Acids); 0 (DNA, Bacterial); 57-92-1 (Streptomycin)

Record Date Created: 19760220

Record Date Completed: 19760220

6/9/54 (Item 5 from file: 5)

0005561335 BIOSIS NO.: 198783040226

DNA **RELATEDNESS AMONG NEISSERIA-** GONORRHOEAE **NEISSERIA-** MENINGITIDIS **NEISSERIA-** LACTAMICA **NEISSERIA-CINEREA AND NEISSERIA-POLYSACCHAREA**

AUTHOR: GUIBOURDENCHE M (Reprint); POPOFF M Y; RIOU J Y
AUTHOR ADDRESS: LAB NEISSERIA, UNITE D'ECOLOGIE BACTERIENNE, INST PASTEUR, 75724 PARIS CEDEX 15, FR**FRANCE

JOURNAL: Annales de l'Institut Pasteur Microbiology 137B (2): p177-186 1986
ISSN: 0769-2609
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: Deoxyribonucleic acid relatedness studies (S1 nuclease method with DE-81 filters method) indicated that Neisseria **gonorrhoeae** , N. **meningitidis** , N. **lactamica** and "N. polysaccharea" form a single genospecies, in which four subspecies can be delineated. However, from a clinical and practical viewpoint, it seems desirable to maintain N. **gonorrhoeae** , N. **meningitidis** , N. **lactamica** and "N. polysaccharea" as separate species. N. cinerea is a valid species, closely related to N. **gonorrhoeae** , N. **meningitidis** , N. **lactamica** and "N. polysaccharea". These five species were 0 to 46 % related to the other known species of the genus Neisseria.

DESCRIPTORS:

MAJOR CONCEPTS: Biochemistry and Molecular Biophysics; Genetics; Infection; Physiology; Systematics and Taxonomy
BIOSYSTEMATIC NAMES: Neisseriaceae--Gram-Negative Aerobic Rods and Cocci, Eubacteria, Bacteria, Microorganisms
COMMON TAXONOMIC TERMS: Bacteria; Eubacteria; Microorganisms
CONCEPT CODES:
00504 General biology - Taxonomy, nomenclature and terminology
10010 Comparative biochemistry
10062 Biochemistry studies - Nucleic acids, purines and pyrimidines
30000 Bacteriology, general and systematic
31000 Physiology and biochemistry of bacteria
31500 Genetics of bacteria and viruses
36002 Medical and clinical microbiology - Bacteriology
BIOSYSTEMATIC CODES:
06507 Neisseriaceae
?t s6/3,kwic/24-49 66 69 77 78 88 97

6/3,KWIC/24 (Item 1 from file: 654)
DIALOG(R)File 654:US Pat.Full.

3652371
Derwent Accession: 1995-115461
Utility
C/ Oligonucleotides **and methods for the detection of Neisseria gonorrhoeae**
Inventor: Birkenmeyer, Larry G., Chicago, IL
Ching, Shanfun, Libertyville, IL
Ohhashi, Yoshihiro, Gurnee, IL
Winkler, Janet K., Lindenhurst, IL
Assignee: Abbott Laboratories (02), Abbott Park, IL
Abbott Laboratories (Code: 00152)
Examiner: Parr, Margaret (Art Unit: 187)
Assistant Examiner: Horlick, Kenneth R.
Combined Principal Attorneys: Brainard, Thomas D.; Yasger, Paul D.

	Publication Number	Kind	Date	Application Number	Filing Date
Main Patent	US 5453355	A	19950926	US 93116388	19930903
CIP	Pen				